



#4

1

# SEQUENCE LISTING

<110> Sprecher, Cindy A.  
Novak, Julia E.  
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Presnell, Scott R.  
Holly, Richard D.  
Nelson, Andrew J.

<120> SOLUBLE ZALPHA11 CYTOKINE RECEPTORS

<130> 00-22

<150> US 60/194,731

<151> 2000-04-05

<150> US 60/222,121

<151> 2000-07-28

<160> 86

<170> FastSEQ for Windows Version 3.0

<210> 1

<211> 1614

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(1614)

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ggc tgg ggc tgc ccc gac ctc gtc tgc tac acc gat tac ctc cag acg	96
Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr	
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gtc atc tgc atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc acc Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr 35 40 45	144
ctt acc tgg caa gac cag tat gaa gag ctg aag gac gag gcc acc tcc Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser 50 55 60	192
tgc agc ctc cac agg tcg gcc cac aat gcc acg cat gcc acc tac acc Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr 65 70 75 80	240
tgc cac atg gat gta ttc cac ttc atg gcc gac gac att ttc agt gtc Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val 85 90 95	288
aac atc aca gac cag tct ggc aac tac tcc cag gag tgt ggc agc ttt Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe 100 105 110	336
ctc ctg gct gag agc atc aag ccg gct ccc cct ttc aac gtg act gtg Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val 115 120 125	384
acc ttc tca gga cag tat aat atc tcc tgg cgc tca gat tac gaa gac Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp 130 135 140	432
cct gcc ttc tac atg ctg aag ggc aag ctt cag tat gag ctg cag tac Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr 145 150 155 160	480
agg aac cgg gga gac ccc tgg gct gtg agt ccg agg aga aag ctg atc Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile 165 170 175	528
tca gtg gac tca aga agt gtc tcc ctc ctc ccc ctg gag ttc cgc aaa Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys 180 185 190	576

gac tcg agc tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc tcc Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser 195 200 205	624
tcc tac cag ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt cag Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln 210 215 220	672
acc cag tca gag gag tta aag gaa ggc tgg aac cct cac ctg ctg ctt Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu 225 230 235 240	720
ctc ctc ctg ctt gtc ata gtc ttc att cct gcc ttc tgg agc ctg aag Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys 245 250 255	768
acc cat cca ttg tgg agg cta tgg aag aag ata tgg gcc gtc ccc agc Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser 260 265 270	816
cct gag cgg ttc ttc atg ccc ctg tac aag ggc tgc agc gga gac ttc Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe 275 280 285	864
aag aaa tgg gtg ggt gca ccc ttc act ggc tcc agc ctg gag ctg gga Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly 290 295 300	912
ccc tgg agc cca gag gtg ccc tcc acc ctg gag gtg tac agc tgc cac Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His 305 310 315 320	960
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cca gca gag ctg gtg gag tct gac ggt gtg ccc aag ccc agc ttc tgg Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp 340 345 350	1056
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Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala	
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gag ggg cca tgc acc tgg ccc tgc agc tgt gag gat gac ggc tac cca	1200
Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro	
385 390 395 400	
gcc ctg gac ctg gat gct ggc ctg gag ccc agc cca ggc cta gag gac	1248
Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp	
405 410 415	
cca ctc ttg gat gca ggg acc aca gtc ctg tcc tgt ggc tgt gtc tca	1296
Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser	
420 425 430	
gct ggc agc cct ggg cta gga ggg ccc ctg gga agc ctc ctg gac aga	1344
Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg	
435 440 445	
cta aag cca ccc ctt gca gat ggg gag gac tgg gct ggg gga ctg ccc	1392
Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro	
450 455 460	
tgg ggt ggc cgg tca cct gga ggg gtc tca gag agt gag gcg ggc tca	1440
Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser	
465 470 475 480	
ccc ctg gcc ggc ctg gat atg gac acg ttt gac agt ggc ttt gtg ggc	1488
Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly	
485 490 495	
tct gac tgc agc agc cct gtg gag tgt gac ttc acc agc ccc ggg gac	1536
Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp	
500 505 510	
gaa gga ccc ccc cgg agc tac ctc cgc cag tgg gtg gtc att cct ccg	1584
Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro	
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1614

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 <211> 538  
 <212> PRT  
 <213> Homo sapiens

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 20 25 30  
 Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr  
 35 40 45  
 Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser  
 50 55 60  
 Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr  
 65 70 75 80  
 Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val  
 85 90 95  
 Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe  
 100 105 110  
 Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val  
 115 120 125  
 Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp  
 130 135 140  
 Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr  
 145 150 155 160  
 Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile  
 165 170 175  
 Ser Val Asp Ser Arg Ser Val Ser Leu Pro Leu Glu Phe Arg Lys  
 180 185 190  
 Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser  
 195 200 205  
 Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln  
 210 215 220  
 Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Leu Leu Leu  
 225 230 235 240  
 Leu Leu Leu Leu Val Ile Val Phe Ile Pro Ala Phe Trp Ser Leu Lys  
 245 250 255

Thr His Pro Leu Trp Arg Leu Trp Lys Lys Ile Trp Ala Val Pro Ser  
 260 265 270  
 Pro Glu Arg Phe Phe Met Pro Leu Tyr Lys Gly Cys Ser Gly Asp Phe  
 275 280 285  
 Lys Lys Trp Val Gly Ala Pro Phe Thr Gly Ser Ser Leu Glu Leu Gly  
 290 295 300  
 Pro Trp Ser Pro Glu Val Pro Ser Thr Leu Glu Val Tyr Ser Cys His  
 305 310 315 320  
 Pro Pro Arg Ser Pro Ala Lys Arg Leu Gln Leu Thr Glu Leu Gln Glu  
 325 330 335  
 Pro Ala Glu Leu Val Glu Ser Asp Gly Val Pro Lys Pro Ser Phe Trp  
 340 345 350  
 Pro Thr Ala Gln Asn Ser Gly Gly Ser Ala Tyr Ser Glu Glu Arg Asp  
 355 360 365  
 Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr Val Leu Asp Ala  
 370 375 380  
 Glu Gly Pro Cys Thr Trp Pro Cys Ser Cys Glu Asp Asp Gly Tyr Pro  
 385 390 395 400  
 Ala Leu Asp Leu Asp Ala Gly Leu Glu Pro Ser Pro Gly Leu Glu Asp  
 405 410 415  
 Pro Leu Leu Asp Ala Gly Thr Thr Val Leu Ser Cys Gly Cys Val Ser  
 420 425 430  
 Ala Gly Ser Pro Gly Leu Gly Gly Pro Leu Gly Ser Leu Leu Asp Arg  
 435 440 445  
 Leu Lys Pro Pro Leu Ala Asp Gly Glu Asp Trp Ala Gly Gly Leu Pro  
 450 455 460  
 Trp Gly Gly Arg Ser Pro Gly Gly Val Ser Glu Ser Glu Ala Gly Ser  
 465 470 475 480  
 Pro Leu Ala Gly Leu Asp Met Asp Thr Phe Asp Ser Gly Phe Val Gly  
 485 490 495  
 Ser Asp Cys Ser Ser Pro Val Glu Cys Asp Phe Thr Ser Pro Gly Asp  
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 Glu Gly Pro Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Ile Pro Pro  
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<210> 3

<211> 696

<212> DNA

<213> Homo sapiens

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(696)

&lt;400&gt; 3

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Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly Asn Glu Asp Thr Thr Ala	
1 5 10 15	
gat ttc ttc ctg acc act atg ccc act gac tcc ctc agt gtt tcc act	96
Asp Phe Phe Leu Thr Thr Met Pro Thr Asp Ser Leu Ser Val Ser Thr	
20 25 30	
ctg ccc ctc cca gag gtt cag tgt ttt gtg ttc aat gtc gag tac atg	144
Leu Pro Leu Pro Glu Val Gln Cys Phe Val Phe Asn Val Glu Tyr Met	
35 40 45	
aat tgc act tgg aac agc agc tct gag ccc cag cct acc aac ctc act	192
Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro Gln Pro Thr Asn Leu Thr	
50 55 60	
ctg cat tat tgg tac aag aac tcg gat aat gat aaa gtc cag aag tgc	240
Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn Asp Lys Val Gln Lys Cys	
65 70 75 80	
agc cac tat cta ttc tct gaa gaa atc act tct ggc tgt cag ttg caa	288
Ser His Tyr Leu Phe Ser Glu Glu Ile Thr Ser Gly Cys Gln Leu Gln	
85 90 95	
aaa aag gag atc cac ctc tac caa aca ttt gtt gtt cag ctc cag gac	336
Lys Lys Glu Ile His Leu Tyr Gln Thr Phe Val Val Gln Leu Gln Asp	
100 105 110	
cca cgg gaa ccc agg aga cag gcc aca cag atg cta aaa ctg cag aat	384
Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln Met Leu Lys Leu Gln Asn	
115 120 125	
ctg gtg atc ccc tgg gct cca gag aac cta aca ctt cac aaa ctg agt	432
Leu Val Ile Pro Trp Ala Pro Glu Asn Leu Thr Leu His Lys Leu Ser	
130 135 140	

gaa tcc cag cta gaa ctg aac tgg aac aac aga ttc ttg aac cac tgt 480  
 Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn Arg Phe Leu Asn His Cys  
 145 150 155 160

ttg gag cac ttg gtg cag tac cgg act gac tgg gac cac agc tgg act 528  
 Leu Glu His Leu Val Gln Tyr Arg Thr Asp Trp Asp His Ser Trp Thr  
 165 170 175

gaa caa tca gtg gat tat aga cat aag ttc tcc ttg cct agt gtg gat 576  
 Glu Gln Ser Val Asp Tyr Arg His Lys Phe Ser Leu Pro Ser Val Asp  
 180 185 190

ggg cag aaa cgc tac acg ttt cgt gtt cgg agc cgc ttt aac cca ctc 624  
 Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg Ser Arg Phe Asn Pro Leu  
 195 200 205

tgt gga agt gct cag cat tgg agt gaa tgg agc cac cca atc cac tgg 672  
 Cys Gly Ser Ala Gln His Trp Ser Glu Trp Ser His Pro Ile His Trp  
 210 215 220

ggg agc aat act tca aaa gag aat 696  
 Gly Ser Asn Thr Ser Lys Glu Asn  
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<210> 4

<211> 232

<212> PRT

<213> Homo sapiens

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 20 25 30  
 Leu Pro Leu Pro Glu Val Gln Cys Phe Val Phe Asn Val Glu Tyr Met  
 35 40 45  
 Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro Gln Pro Thr Asn Leu Thr  
 50 55 60  
 Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn Asp Lys Val Gln Lys Cys  
 65 70 75 80  
 Ser His Tyr Leu Phe Ser Glu Glu Ile Thr Ser Gly Cys Gln Leu Gln  
 85 90 95



Lys Lys Glu Ile His Leu Tyr Gln Thr Phe Val Val Gln Leu Gln Asp  
 100 105 110  
 Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln Met Leu Lys Leu Gln Asn  
 115 120 125  
 Leu Val Ile Pro Trp Ala Pro Glu Asn Leu Thr Leu His Lys Leu Ser  
 130 135 140  
 Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn Arg Phe Leu Asn His Cys  
 145 150 155 160  
 Leu Glu His Leu Val Gln Tyr Arg Thr Asp Trp Asp His Ser Trp Thr  
 165 170 175  
 Glu Gln Ser Val Asp Tyr Arg His Lys Phe Ser Leu Pro Ser Val Asp  
 180 185 190  
 Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg Ser Arg Phe Asn Pro Leu  
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 Cys Gly Ser Ala Gln His Trp Ser Glu Trp Ser His Pro Ile His Trp  
 210 215 220  
 Gly Ser Asn Thr Ser Lys Glu Asn  
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<210> 5  
 <211> 654  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(654)

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1 5 10 15	
atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc acc ctt acc tgg	96
Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr Leu Thr Trp	
20 25 30	
caa gac cag tat gaa gag ctg aag gac gag gcc acc tcc tgc agc ctc	144
Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu	
35 40 45	

cac agg tcg gcc cac aat gcc acg cat gcc acc tac acc tgc cac atg His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr Cys His Met 50 55 60	192
gat gta ttc cac ttc atg gcc gac gac att ttc agt gtc aac atc aca Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr 65 70 75 80	240
gac cag tct ggc aac tac tcc cag gag tgt ggc agc ttt ctc ctg gct Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala 85 90 95	288
gag agc atc aag ccg gct ccc cct ttc aac gtg act gtg acc ttc tca Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val Thr Phe Ser 100 105 110	336
gga cag tat aat atc tcc tgg cgc tca gat tac gaa gac cct gcc ttc Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala Phe 115 120 125	384
tac atg ctg aag ggc aag ctt cag tat gag ctg cag tac agg aac cgg Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Arg 130 135 140	432
gga gac ccc tgg gct gtg agt ccg agg aga aag ctg atc tca gtg gac Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val Asp 145 150 155 160	480
tca aga agt gtc tcc ctc ctc ccc ctg gag ttc cgc aaa gac tcg agc Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser 165 170 175	528
tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc tcc tcc tac cag Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln 180 185 190	576
ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt cag acc cag tca Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser 195 200 205	624
gag gag tta aag gaa ggc tgg aac cct cac Glu Glu Leu Lys Glu Gly Trp Asn Pro His 210 215	654

<210> 6  
 <211> 218  
 <212> PRT  
 <213> Homo sapiens

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 20 25 30  
 Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu  
 35 40 45  
 His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr Cys His Met  
 50 55 60  
 Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr  
 65 70 75 80  
 Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala  
 85 90 95  
 Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val Thr Phe Ser  
 100 105 110  
 Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala Phe  
 115 120 125  
 Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Arg  
 130 135 140  
 Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val Asp  
 145 150 155 160  
 Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser  
 165 170 175  
 Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln  
 180 185 190  
 Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser  
 195 200 205  
 Glu Glu Leu Lys Glu Gly Trp Asn Pro His  
 210 215

<210> 7  
 <211> 654  
 <212> DNA  
 <213> Artificial Sequence

<220>

<223> Degenerate polynucleotide sequence of soluble  
zalpall Receptor polypeptide as shown in SEQ ID  
NO:6

<221> misc\_feature

<222> (1)...(654)

<223> n = A,T,C or G

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gaygargcna	cnwsntgyws	nytncaymgn	wsngcncaya	aygcnacnca	ygcnacntay	180
acntgycaya	tggaygtntt	ycayttyatg	gcngaygaya	thttywsngt	naayathacn	240
gaycarwsng	gnaaytayws	ncargartgy	ggnwsnttyy	tnytngcnga	rwsnathaar	300
ccngcncnc	cnttyaaygt	nacngtnacn	ttywsnggnc	artayaayat	hwsntggmgn	360
wsngaytayg	argayccngc	nttytayatg	ytnaarggna	arytncarta	ygarytncar	420
taymgnaaym	gnggngaycc	ntgggcngtn	wsnccnmgnm	gnaarytnat	hwsngtngay	480
wsnmgnwsng	tnwsnytnyt	nccnytngar	ttymgnaarg	aywsnwsnta	ygarytncar	540
gtnmngncng	gnccnatgcc	nggnwsnwsn	taycarggna	cntggwsnga	rtggwsngay	600
ccngtnatht	tycaracnca	rwsngargar	ytnaargarg	gntggaaycc	ncay	654

<210> 8

<211> 696

<212> DNA

<213> Artificial Sequence

<220>

<223> Degenerate polynucleotide sequence of IL-2Rgamma  
polypeptide as shown in SEQ ID NO:4

<221> misc\_feature

<222> (1)...(696)

<223> n = A,T,C or G

<400> 8

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ttygtnttya	aygtngarta	yatgaaytgy	acntggaayw	snwsnwsnga	rccncarccn	180
acnaayytna	cnytncayta	ytggtayaar	aaywsngaya	aygayaargt	ncaraartgy	240
wsncaytayy	tnttywsnga	rgarathacn	wsnggntgyc	arytncaraa	raargarath	300
cayytntayc	aracnttygt	ngtnarytn	cargayccnm	gngarccnmg	nmgncargcn	360
acncaratgy	tnaarytnca	raayytngtn	athccntggg	cncngaraa	yytnacnytn	420

cayaarytnw sngarwsnca rytngarytn aaytggaaya aymgnttyyt naaycaytgy	480
ytngarcayy tngtncarta ymgnacngay tgggaycayw sntggacnga rcarwsngtn	540
gaytaymgnc ayaarttyws nytnccnwsn gtngayggnc araarmgnta yacnttymgn	600
gtnmgnwsnm gnttyaaycc nytnthygggn wsnegncarc aytggwsnga rtggwsncay	660
ccnathcayt ggggnwsnaa yacnwsnaar garaay	696

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 <212> DNA  
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<220>  
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 <222> (1)...(486)

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1				5				10					15			
gtc	atc	ttc	ttg	ggg	aca	ctg	gtc	cac	aaa	tca	agc	tcc	caa	ggg	caa	96
Val	Ile	Phe	Leu	Gly	Thr	Leu	Val	His	Lys	Ser	Ser	Ser	Gln	Gly	Gln	
			20					25					30			
gat	cgc	cac	atg	att	aga	atg	cgt	caa	ctt	ata	gat	att	gtt	gat	cag	144
Asp	Arg	His	Met	Ile	Arg	Met	Arg	Gln	Leu	Ile	Asp	Ile	Val	Asp	Gln	
		35					40					45				
ctg	aaa	aat	tat	gtg	aat	gac	ttg	gtc	cct	gaa	ttt	ctg	cca	gct	cca	192
Leu	Lys	Asn	Tyr	Val	Asn	Asp	Leu	Val	Pro	Glu	Phe	Leu	Pro	Ala	Pro	
	50					55				60						
gaa	gat	gta	gag	aca	aac	tgt	gag	tgg	tca	gct	ttt	tcc	tgt	ttt	cag	240
Glu	Asp	Val	Glu	Thr	Asn	Cys	Glu	Trp	Ser	Ala	Phe	Ser	Cys	Phe	Gln	
65					70				75					80		
aag	gcc	caa	cta	aag	tca	gca	aat	aca	gga	aac	aat	gaa	agg	ata	atc	288
Lys	Ala	Gln	Leu	Lys	Ser	Ala	Asn	Thr	Gly	Asn	Asn	Glu	Arg	Ile	Ile	
			85					90					95			
aat	gta	tca	att	aaa	aag	ctg	aag	agg	aaa	cca	cct	tcc	aca	aat	gca	336
Asn	Val	Ser	Ile	Lys	Lys	Leu	Lys	Arg	Lys	Pro	Pro	Ser	Thr	Asn	Ala	
			100					105					110			

ggg aga aga cag aaa cac aga cta aca tgc cct tca tgt gat tct tat	384
Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys Asp Ser Tyr	
115 120 125	
gag aaa aaa cca ccc aaa gaa ttc cta gaa aga ttc aaa tca ctt ctc	432
Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys Ser Leu Leu	
130 135 140	
caa aag atg att cat cag cat ctg tcc tct aga aca cac gga agt gaa	480
Gln Lys Met Ile His Gln His Leu Ser Ser Arg Thr His Gly Ser Glu	
145 150 155 160	
gat tcc	486
Asp Ser	

<210> 10  
 <211> 162  
 <212> PRT  
 <213> Homo sapiens

<400> 10

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Val Ile Phe Leu Gly Thr Leu Val His Lys Ser Ser Ser Gln Gly Gln	
20 25 30	
Asp Arg His Met Ile Arg Met Arg Gln Leu Ile Asp Ile Val Asp Gln	
35 40 45	
Leu Lys Asn Tyr Val Asn Asp Leu Val Pro Glu Phe Leu Pro Ala Pro	
50 55 60	
Glu Asp Val Glu Thr Asn Cys Glu Trp Ser Ala Phe Ser Cys Phe Gln	
65 70 75 80	
Lys Ala Gln Leu Lys Ser Ala Asn Thr Gly Asn Asn Glu Arg Ile Ile	
85 90 95	
Asn Val Ser Ile Lys Lys Leu Lys Arg Lys Pro Pro Ser Thr Asn Ala	
100 105 110	
Gly Arg Arg Gln Lys His Arg Leu Thr Cys Pro Ser Cys Asp Ser Tyr	
115 120 125	
Glu Lys Lys Pro Pro Lys Glu Phe Leu Glu Arg Phe Lys Ser Leu Leu	
130 135 140	

Gln Lys Met Ile His Gln His Leu Ser Ser Arg Thr His Gly Ser Glu  
 145 150 155 160  
 Asp Ser

<210> 11  
 <211> 1735  
 <212> DNA  
 <213> mus musculus

<220>  
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 <222> (143)...(1729)

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 aggagtaggt ctgggacaca gc atg ccc cgg ggc cca gtg gct gcc tta ctc 172  
 Met Pro Arg Gly Pro Val Ala Ala Leu Leu  
 1 5 10

ctg ctg att ctc cat gga gct tgg agc tgc ctg gac ctc act tgc tac 220  
 Leu Leu Ile Leu His Gly Ala Trp Ser Cys Leu Asp Leu Thr Cys Tyr  
 15 20 25

act gac tac ctc tgg acc atc acc tgt gtc ctg gag aca cgg agc ccc 268  
 Thr Asp Tyr Leu Trp Thr Ile Thr Cys Val Leu Glu Thr Arg Ser Pro  
 30 35 40

aac ccc agc ata ctc agt ctc acc tgg caa gat gaa tat gag gaa ctt 316  
 Asn Pro Ser Ile Leu Ser Leu Thr Trp Gln Asp Glu Tyr Glu Glu Leu  
 45 50 55

cag gac caa gag acc ttc tgc agc cta cac agg tct ggc cac aac acc 364  
 Gln Asp Gln Glu Thr Phe Cys Ser Leu His Arg Ser Gly His Asn Thr  
 60 65 70

aca cat ata tgg tac acg tgc cat atg cgc ttg tct caa ttc ctg tcc 412  
 Thr His Ile Trp Tyr Thr Cys His Met Arg Leu Ser Gln Phe Leu Ser  
 75 80 85 90

gat gaa gtt ttc att gtc aat gtg acg gac cag tct ggc aac aac tcc	460
Asp Glu Val Phe Ile Val Asn Val Thr Asp Gln Ser Gly Asn Asn Ser	
95 100 105	
caa gag tgt ggc agc ttt gtc ctg gct gag agc atc aaa cca gct ccc	508
Gln Glu Cys Gly Ser Phe Val Leu Ala Glu Ser Ile Lys Pro Ala Pro	
110 115 120	
ccc ttg aac gtg act gtg gcc ttc tca gga cgc tat gat atc tcc tgg	556
Pro Leu Asn Val Thr Val Ala Phe Ser Gly Arg Tyr Asp Ile Ser Trp	
125 130 135	
gac tca gct tat gac gaa ccc tcc aac tac gtg ctg agg ggc aag cta	604
Asp Ser Ala Tyr Asp Glu Pro Ser Asn Tyr Val Leu Arg Gly Lys Leu	
140 145 150	
caa tat gag ctg cag tat cgg aac ctc aga gac ccc tat gct gtg agg	652
Gln Tyr Glu Leu Gln Tyr Arg Asn Leu Arg Asp Pro Tyr Ala Val Arg	
155 160 165 170	
ccg gtg acc aag ctg atc tca gtg gac tca aga aac gtc tct ctt ctc	700
Pro Val Thr Lys Leu Ile Ser Val Asp Ser Arg Asn Val Ser Leu Leu	
175 180 185	
cct gaa gag ttc cac aaa gat tct agc tac cag ctg cag gtg cgg gca	748
Pro Glu Glu Phe His Lys Asp Ser Ser Tyr Gln Leu Gln Val Arg Ala	
190 195 200	
gcg cct cag cca ggc act tca ttc agg ggg acc tgg agt gag tgg agt	796
Ala Pro Gln Pro Gly Thr Ser Phe Arg Gly Thr Trp Ser Glu Trp Ser	
205 210 215	
gac ccc gtc atc ttt cag acc cag gct ggg gag ccc gag gca ggc tgg	844
Asp Pro Val Ile Phe Gln Thr Gln Ala Gly Glu Pro Glu Ala Gly Trp	
220 225 230	
gac cct cac atg ctg ctg ctc ctg gct gtc ttg atc att gtc ctg gtt	892
Asp Pro His Met Leu Leu Leu Leu Ala Val Leu Ile Ile Val Leu Val	
235 240 245 250	
ttc atg ggt ctg aag atc cac ctg cct tgg agg cta tgg aaa aag ata	940
Phe Met Gly Leu Lys Ile His Leu Pro Trp Arg Leu Trp Lys Lys Ile	
255 260 265	



tgg gca cca gtg ccc acc cct gag agt ttc ttc cag ccc ctg tac agg	988
Trp Ala Pro Val Pro Thr Pro Glu Ser Phe Phe Gln Pro Leu Tyr Arg	
270 275 280	
gag cac agc ggg aac ttc aag aaa tgg gtt aat acc cct ttc acg gcc	1036
Glu His Ser Gly Asn Phe Lys Lys Trp Val Asn Thr Pro Phe Thr Ala	
285 290 295	
tcc agc ata gag ttg gtg cca cag agt tcc aca aca aca tca gcc tta	1084
Ser Ser Ile Glu Leu Val Pro Gln Ser Ser Thr Thr Thr Ser Ala Leu	
300 305 310	
cat ctg tca ttg tat cca gcc aag gag aag aag ttc ccg ggg ctg ccg	1132
His Leu Ser Leu Tyr Pro Ala Lys Glu Lys Lys Phe Pro Gly Leu Pro	
315 320 325 330	
ggt ctg gaa gag caa ctg gag tgt gat gga atg tct gag cct ggt cac	1180
Gly Leu Glu Glu Gln Leu Glu Cys Asp Gly Met Ser Glu Pro Gly His	
335 340 345	
tgg tgc ata atc ccc ttg gca gct ggc caa gcg gtc tca gcc tac agt	1228
Trp Cys Ile Ile Pro Leu Ala Ala Gly Gln Ala Val Ser Ala Tyr Ser	
350 355 360	
gag gag aga gac cgg cca tat ggt ctg gtg tcc att gac aca gtg act	1276
Glu Glu Arg Asp Arg Pro Tyr Gly Leu Val Ser Ile Asp Thr Val Thr	
365 370 375	
gtg gga gat gca gag ggc ctg tgt gtc tgg ccc tgt agc tgt gag gat	1324
Val Gly Asp Ala Glu Gly Leu Cys Val Trp Pro Cys Ser Cys Glu Asp	
380 385 390	
gat ggc tat cca gcc atg aac ctg gat gct ggc cga gag tct ggc cct	1372
Asp Gly Tyr Pro Ala Met Asn Leu Asp Ala Gly Arg Glu Ser Gly Pro	
395 400 405 410	
aat tca gag gat ctg ctc ttg gtc aca gac cct gct ttt ctg tct tgc	1420
Asn Ser Glu Asp Leu Leu Leu Val Thr Asp Pro Ala Phe Leu Ser Cys	
415 420 425	

ggc tgt gtc tca ggt agt ggt ctc agg ctt gga ggc tcc cca ggc agc 1468  
Gly Cys Val Ser Gly Ser Gly Leu Arg Leu Gly Gly Ser Pro Gly Ser  
430 435 440

cta ctg gac agg ttg agg ctg tca ttt gca aag gaa ggg gac tgg aca 1516  
Leu Leu Asp Arg Leu Arg Leu Ser Phe Ala Lys Glu Gly Asp Trp Thr  
445 450 455

gca gac cca acc tgg aga act ggg tcc cca gga ggg ggc tct gag agt 1564  
Ala Asp Pro Thr Trp Arg Thr Gly Ser Pro Gly Gly Gly Ser Glu Ser  
460 465 470

gaa gca ggt tcc ccc cct ggt ctg gac atg gac aca ttt gac agt ggc 1612  
Glu Ala Gly Ser Pro Pro Gly Leu Asp Met Asp Thr Phe Asp Ser Gly  
475 480 485 490

ttt gca ggt tca gac tgt ggc agc ccc gtg gag act gat gaa gga ccc 1660  
Phe Ala Gly Ser Asp Cys Gly Ser Pro Val Glu Thr Asp Glu Gly Pro  
495 500 505

cct cga agc tat ctc cgc cag tgg gtg gtc agg acc cct cca cct gtg 1708  
Pro Arg Ser Tyr Leu Arg Gln Trp Val Val Arg Thr Pro Pro Pro Val  
510 515 520

gac agt gga gcc cag agc agc tagcat 1735  
Asp Ser Gly Ala Gln Ser Ser  
525

<210> 12  
<211> 529  
<212> PRT  
<213> mus musculus

<400> 12															
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Ala	Trp	Ser	Cys	Leu	Asp	Leu	Thr	Cys	Tyr	Thr	Asp	Tyr	Leu	Trp	Thr
			20					25					30		
Ile	Thr	Cys	Val	Leu	Glu	Thr	Arg	Ser	Pro	Asn	Pro	Ser	Ile	Leu	Ser
		35					40					45			
Leu	Thr	Trp	Gln	Asp	Glu	Tyr	Glu	Glu	Leu	Gln	Asp	Gln	Glu	Thr	Phe
	50					55					60				

Cys	Ser	Leu	His	Arg	Ser	Gly	His	Asn	Thr	Thr	His	Ile	Trp	Tyr	Thr	65	70	75	80
Cys	His	Met	Arg	Leu	Ser	Gln	Phe	Leu	Ser	Asp	Glu	Val	Phe	Ile	Val	85	90	95	
Asn	Val	Thr	Asp	Gln	Ser	Gly	Asn	Asn	Ser	Gln	Glu	Cys	Gly	Ser	Phe	100	105	110	
Val	Leu	Ala	Glu	Ser	Ile	Lys	Pro	Ala	Pro	Pro	Leu	Asn	Val	Thr	Val	115	120	125	
Ala	Phe	Ser	Gly	Arg	Tyr	Asp	Ile	Ser	Trp	Asp	Ser	Ala	Tyr	Asp	Glu	130	135	140	
Pro	Ser	Asn	Tyr	Val	Leu	Arg	Gly	Lys	Leu	Gln	Tyr	Glu	Leu	Gln	Tyr	145	150	155	160
Arg	Asn	Leu	Arg	Asp	Pro	Tyr	Ala	Val	Arg	Pro	Val	Thr	Lys	Leu	Ile	165	170	175	
Ser	Val	Asp	Ser	Arg	Asn	Val	Ser	Leu	Leu	Pro	Glu	Glu	Phe	His	Lys	180	185	190	
Asp	Ser	Ser	Tyr	Gln	Leu	Gln	Val	Arg	Ala	Ala	Pro	Gln	Pro	Gly	Thr	195	200	205	
Ser	Phe	Arg	Gly	Thr	Trp	Ser	Glu	Trp	Ser	Asp	Pro	Val	Ile	Phe	Gln	210	215	220	
Thr	Gln	Ala	Gly	Glu	Pro	Glu	Ala	Gly	Trp	Asp	Pro	His	Met	Leu	Leu	225	230	235	240
Leu	Leu	Ala	Val	Leu	Ile	Ile	Val	Leu	Val	Phe	Met	Gly	Leu	Lys	Ile	245	250	255	
His	Leu	Pro	Trp	Arg	Leu	Trp	Lys	Lys	Ile	Trp	Ala	Pro	Val	Pro	Thr	260	265	270	
Pro	Glu	Ser	Phe	Phe	Gln	Pro	Leu	Tyr	Arg	Glu	His	Ser	Gly	Asn	Phe	275	280	285	
Lys	Lys	Trp	Val	Asn	Thr	Pro	Phe	Thr	Ala	Ser	Ser	Ile	Glu	Leu	Val	290	295	300	
Pro	Gln	Ser	Ser	Thr	Thr	Thr	Ser	Ala	Leu	His	Leu	Ser	Leu	Tyr	Pro	305	310	315	320
Ala	Lys	Glu	Lys	Lys	Phe	Pro	Gly	Leu	Pro	Gly	Leu	Glu	Glu	Gln	Leu	325	330	335	
Glu	Cys	Asp	Gly	Met	Ser	Glu	Pro	Gly	His	Trp	Cys	Ile	Ile	Pro	Leu	340	345	350	
Ala	Ala	Gly	Gln	Ala	Val	Ser	Ala	Tyr	Ser	Glu	Glu	Arg	Asp	Arg	Pro	355	360	365	
Tyr	Gly	Leu	Val	Ser	Ile	Asp	Thr	Val	Thr	Val	Gly	Asp	Ala	Glu	Gly	370	375	380	
Leu	Cys	Val	Trp	Pro	Cys	Ser	Cys	Glu	Asp	Asp	Gly	Tyr	Pro	Ala	Met	385	390	395	400

Asn	Leu	Asp	Ala	Gly	Arg	Glu	Ser	Gly	Pro	Asn	Ser	Glu	Asp	Leu	Leu
				405				410				415			
Leu	Val	Thr	Asp	Pro	Ala	Phe	Leu	Ser	Cys	Gly	Cys	Val	Ser	Gly	Ser
				420				425				430			
Gly	Leu	Arg	Leu	Gly	Gly	Ser	Pro	Gly	Ser	Leu	Leu	Asp	Arg	Leu	Arg
				435				440				445			
Leu	Ser	Phe	Ala	Lys	Glu	Gly	Asp	Trp	Thr	Ala	Asp	Pro	Thr	Trp	Arg
				450				455				460			
Thr	Gly	Ser	Pro	Gly	Gly	Gly	Ser	Glu	Ser	Glu	Ala	Gly	Ser	Pro	Pro
465				470				475				480			
Gly	Leu	Asp	Met	Asp	Thr	Phe	Asp	Ser	Gly	Phe	Ala	Gly	Ser	Asp	Cys
				485				490				495			
Gly	Ser	Pro	Val	Glu	Thr	Asp	Glu	Gly	Pro	Pro	Arg	Ser	Tyr	Leu	Arg
				500				505				510			
Gln	Trp	Val	Val	Arg	Thr	Pro	Pro	Pro	Val	Asp	Ser	Gly	Ala	Gln	Ser
				515				520				525			
Ser															

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<210> 13
<211> 5
<212> PRT
<213> Artificial Sequence
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<220>  
<223> WSXWS polypeptide consensus motif

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<221> VARIANT
<222> (1)...(5)
<223> Xaa = Any Amino Acid
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<400> 13  
Trp Ser Xaa Trp Ser  
1 5

<210> 14  
<211> 6  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Glu-Glu (CEE) Tag amino acid sequence

<400> 14  
 Glu Tyr Met Pro Met Glu  
 1 5

<210> 15  
 <211> 1701  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> soluble zalpha11R/IgGgamma1 construct

<221> CDS  
 <222> (1)...(1701)

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 atg ccg cgt ggc tgg gcc gcc ccc ttg ctc ctg ctg ctg ctc cag gga 48  
 Met Pro Arg Gly Trp Ala Ala Pro Leu Leu Leu Leu Leu Gln Gly  
 1 5 10 15

ggc tgg ggc tgc ccc gac ctc gtc tgc tac acc gat tac ctc cag acg 96  
 Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln Thr  
 20 25 30

gtc atc tgc atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc acc 144  
 Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu Thr  
 35 40 45

ctt acc tgg caa gac cag tat gaa gag ctg aag gac gag gcc acc tcc 192  
 Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr Ser  
 50 55 60

tgc agc ctc cac agg tcg gcc cac aat gcc acg cat gcc acc tac acc 240  
 Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr Thr  
 65 70 75 80

tgc cac atg gat gta ttc cac ttc atg gcc gac gac att ttc agt gtc 288  
 Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser Val  
 85 90 95

aac atc aca gac cag tct ggc aac tac tcc cag gag tgt ggc agc ttt 336  
 Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser Phe  
 100 105 110

ctc ctg gct gag agc atc aag ccg gct ccc cct ttc aac gtg act gtg Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr Val 115 120 125	384
acc ttc tca gga cag tat aat atc tcc tgg cgc tca gat tac gaa gac Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp 130 135 140	432
cct gcc ttc tac atg ctg aag ggc aag ctt cag tat gag ctg cag tac Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr 145 150 155 160	480
agg aac cgg gga gac ccc tgg gct gtg agt ccg agg aga aag ctg atc Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu Ile 165 170 175	528
tca gtg gac tca aga agt gtc tcc ctc ctc ccc ctg gag ttc cgc aaa Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg Lys 180 185 190	576
gac tcg agc tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc tcc Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly Ser 195 200 205	624
tcc tac cag ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt cag Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln 210 215 220	672
acc cag tca gag gag tta aag gaa ggc tgg aac cct cac gct agc acc Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His Ala Ser Thr 225 230 235 240	720
aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc tcc aag agc acc tct Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser 245 250 255	768
ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag gac tac ttc ccc gaa Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu 260 265 270	816

ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg acc agc ggc gtg cac Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His 275 280 285	864
acc ttc ccg gct gtc cta cag tcc tca gga ctc tac tcc ctc agc agc Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser 290 295 300	912
gtg gtg acc gtg ccc tcc agc agc ttg ggc acc cag acc tac atc tgc Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile Cys 305 310 315 320	960
aac gtg aat cac aag ccc agc aac acc aag gtg gac aag aaa gtt gag Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys Val Glu 325 330 335	1008
ccc aaa tct tgt gac aaa act cac aca tgc cca ccg tgc cca gca cct Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro 340 345 350	1056
gaa ctc ctg ggg gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys 355 360 365	1104
gac acc ctc atg atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val 370 375 380	1152
gac gtg agc cac gaa gac cct gag gtc aag ttc aac tgg tac gtg gac Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp 385 390 395 400	1200
ggc gtg gag gtg cat aat gcc aag aca aag ccg cgg gag gag cag tac Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr 405 410 415	1248
aac agc acg tac cgt gtg gtc agc gtc ctc acc gtc ctg cac cag gac Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp 420 425 430	1296
tgg ctg aat ggc aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu 435 440 445	1344

cca gcc ccc atc gag aaa acc atc tcc aaa gcc aaa ggg cag ccc cga Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg 450 455 460	1392
gaa cca cag gtg tac acc ctg ccc cca tcc cgg gat gag ctg acc aag Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys 465 470 475 480	1440
aac cag gtc agc ctg acc tgc ctg gtc aaa ggc ttc tat ccc agc gac Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp 485 490 495	1488
atc gcc gtg gag tgg gag agc aat ggg cag ccg gag aac aac tac aag Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys 500 505 510	1536
acc acg cct ccc gtg ctg gac tcc gac ggc tcc ttc ttc ctc tac agc Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser 515 520 525	1584
aag ctc acc gtg gac aag agc agg tgg cag cag ggg aac gtc ttc tca Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser 530 535 540	1632
tgc tcc gtg atg cat gag gct ctg cac aac cac tac acg cag aag agc Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser 545 550 555 560	1680
ctc tcc ctg tct ccg ggt aaa Leu Ser Leu Ser Pro Gly Lys 565	1701

&lt;210&gt; 16

&lt;211&gt; 567

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; soluble zalpha11R/IgGgamma1 polypeptide

&lt;400&gt; 16



Met	Pro	Arg	Gly	Trp	Ala	Ala	Pro	Leu	Leu	Leu	Leu	Leu	Leu	Gln	Gly
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			20					25					30		
Val	Ile	Cys	Ile	Leu	Glu	Met	Trp	Asn	Leu	His	Pro	Ser	Thr	Leu	Thr
		35					40					45			
Leu	Thr	Trp	Gln	Asp	Gln	Tyr	Glu	Glu	Leu	Lys	Asp	Glu	Ala	Thr	Ser
	50					55					60				
Cys	Ser	Leu	His	Arg	Ser	Ala	His	Asn	Ala	Thr	His	Ala	Thr	Tyr	Thr
65					70					75					80
Cys	His	Met	Asp	Val	Phe	His	Phe	Met	Ala	Asp	Asp	Ile	Phe	Ser	Val
			85					90					95		
Asn	Ile	Thr	Asp	Gln	Ser	Gly	Asn	Tyr	Ser	Gln	Glu	Cys	Gly	Ser	Phe
			100					105					110		
Leu	Leu	Ala	Glu	Ser	Ile	Lys	Pro	Ala	Pro	Pro	Phe	Asn	Val	Thr	Val
		115					120					125			
Thr	Phe	Ser	Gly	Gln	Tyr	Asn	Ile	Ser	Trp	Arg	Ser	Asp	Tyr	Glu	Asp
	130					135					140				
Pro	Ala	Phe	Tyr	Met	Leu	Lys	Gly	Lys	Leu	Gln	Tyr	Glu	Leu	Gln	Tyr
145					150					155					160
Arg	Asn	Arg	Gly	Asp	Pro	Trp	Ala	Val	Ser	Pro	Arg	Arg	Lys	Leu	Ile
			165					170						175	
Ser	Val	Asp	Ser	Arg	Ser	Val	Ser	Leu	Leu	Pro	Leu	Glu	Phe	Arg	Lys
		180				185						190			
Asp	Ser	Ser	Tyr	Glu	Leu	Gln	Val	Arg	Ala	Gly	Pro	Met	Pro	Gly	Ser
	195					200					205				
Ser	Tyr	Gln	Gly	Thr	Trp	Ser	Glu	Trp	Ser	Asp	Pro	Val	Ile	Phe	Gln
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Thr	Gln	Ser	Glu	Glu	Leu	Lys	Glu	Gly	Trp	Asn	Pro	His	Ala	Ser	Thr
225					230					235					240
Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser
			245					250						255	
Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu
		260					265						270		
Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	His
	275					280						285			
Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser
	290					295					300				
Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys
305					310					315					320
Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu
			325					330						335	

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Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro
      340                      345                      350
Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys
      355                      360                      365
Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val
      370                      375                      380
Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp
385                      390                      395                      400
Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr
      405                      410                      415
Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp
      420                      425                      430
Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu
      435                      440                      445
Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg
      450                      455                      460
Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys
465                      470                      475                      480
Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp
      485                      490                      495
Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys
      500                      505                      510
Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser
      515                      520                      525
Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser
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Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser
545                      550                      555                      560
Leu Ser Leu Ser Pro Gly Lys
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<210> 17

<211> 1083

<212> DNA

<213> Artificial Sequence

<220>

<223> soluble human IL-2Rgamma/human kappa light chain  
construct

<221> CDS

<222> (1)...(1083)

<400> 17

atg ttg aag cca tca tta cca ttc aca tcc ctc tta ttc ctg cag ctg	48
Met Leu Lys Pro Ser Leu Pro Phe Thr Ser Leu Leu Phe Leu Gln Leu	
1 5 10 15	
ccc ctg ctg gga gtg ggg ctg aac acg aca att ctg acg ccc aat ggg	96
Pro Leu Leu Gly Val Gly Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly	
20 25 30	
aat gaa gac acc aca gct gat ttc ttc ctg acc act atg ccc act gac	144
Asn Glu Asp Thr Thr Ala Asp Phe Phe Leu Thr Thr Met Pro Thr Asp	
35 40 45	
tcc ctc agt gtt tcc act ctg ccc ctc cca gag gtt cag tgt ttt gtg	192
Ser Leu Ser Val Ser Thr Leu Pro Leu Pro Glu Val Gln Cys Phe Val	
50 55 60	
ttc aat gtc gag tac atg aat tgc act tgg aac agc agc tct gag ccc	240
Phe Asn Val Glu Tyr Met Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro	
65 70 75 80	
cag cct acc aac ctc act ctg cat tat tgg tac aag aac tcg gat aat	288
Gln Pro Thr Asn Leu Thr Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn	
85 90 95	
gat aaa gtc cag aag tgc agc cac tat cta ttc tct gaa gaa atc act	336
Asp Lys Val Gln Lys Cys Ser His Tyr Leu Phe Ser Glu Glu Ile Thr	
100 105 110	
tct ggc tgt cag ttg caa aaa aag gag atc cac ctc tac caa aca ttt	384
Ser Gly Cys Gln Leu Gln Lys Lys Glu Ile His Leu Tyr Gln Thr Phe	
115 120 125	
gtt gtt cag ctc cag gac cca cgg gaa ccc agg aga cag gcc aca cag	432
Val Val Gln Leu Gln Asp Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln	
130 135 140	
atg cta aaa ctg cag aat ctg gtg atc ccc tgg gct cca gag aac cta	480
Met Leu Lys Leu Gln Asn Leu Val Ile Pro Trp Ala Pro Glu Asn Leu	
145 150 155 160	

28

aca ctt cac aaa ctg agt gaa tcc cag cta gaa ctg aac tgg aac aac 528  
 Thr Leu His Lys Leu Ser Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn  
 165  
 aga ttc ttg aac cac tgt ttg gag cac ttg gtg cag tac cgg act gac 576  
 Arg Phe Leu Asn His Cys Leu Glu His Leu Val Gln Tyr Arg Thr Asp  
 170  
 tgg gac cac agc tgg act gaa caa tca gtg gat tat aga cat aag ttc 624  
 Trp Asp His Ser Trp Thr Glu Gln Ser Val Asp Tyr Arg His Lys Phe  
 185  
 tcc ttg cct agt gtg gat ggg cag aaa cgc tac acg ttt cgt gtt cgg 672  
 Ser Leu Pro Ser Val Asp Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg  
 200  
 agc cgc ttt aac cca ctc tgt gga agt gct cag cat tgg agt gaa tgg 720  
 Ser Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp  
 215  
 agc cac cca atc cac tgg ggg agc aat act tca aaa gag aat act gtg 768  
 Ser His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Thr Val  
 230  
 gct gca cca tct gtc ttc atc ttc ccg cca tct gat gag cag ttg aaa 816  
 Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys  
 245  
 tct ggt acc gcc tct gtt gtg tgc ctg ctg aat aac ttc tat ccc aga 864  
 Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg  
 260  
 gag gcc aaa gta cag tgg aag gtg gat aac gcc ctc caa tcg ggt aac 912  
 Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn  
 280  
 tcc cag gag agt gtc aca gag cag gac agc aag gac agc acc tac agc 960  
 Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser  
 295  
 ctc agc agc acc ctg acg ctg agc aaa gca gac tac gag aaa cac aaa 1008  
 Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys  
 310  
 325  
 330  
 335

gtc tac gcc tgc gaa gtc acc cat cag ggc ctg agc tcg ccc gtc aca 1056  
 Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr  
                   340                                  345                                  350

aag agc ttc aac agg gga gag tgt tag 1083  
 Lys Ser Phe Asn Arg Gly Glu Cys \*  
                   355                                  360

<210> 18

<211> 360

<212> PRT

<213> Artificial Sequence

<220>

<223> soluble human IL-2Rgamma/human kappa light chain  
 polypeptide

<400> 18

Met Leu Lys Pro Ser Leu Pro Phe Thr Ser Leu Leu Phe Leu Gln Leu  
 1                  5                                  10                                  15  
 Pro Leu Leu Gly Val Gly Leu Asn Thr Thr Ile Leu Thr Pro Asn Gly  
                   20                                  25                                  30  
 Asn Glu Asp Thr Thr Ala Asp Phe Phe Leu Thr Thr Met Pro Thr Asp  
                   35                                  40                                  45  
 Ser Leu Ser Val Ser Thr Leu Pro Leu Pro Glu Val Gln Cys Phe Val  
                   50                                  55                                  60  
 Phe Asn Val Glu Tyr Met Asn Cys Thr Trp Asn Ser Ser Ser Glu Pro  
 65                                  70                                  75                                  80  
 Gln Pro Thr Asn Leu Thr Leu His Tyr Trp Tyr Lys Asn Ser Asp Asn  
                   85                                  90                                  95  
 Asp Lys Val Gln Lys Cys Ser His Tyr Leu Phe Ser Glu Glu Ile Thr  
                   100                                  105                                  110  
 Ser Gly Cys Gln Leu Gln Lys Lys Glu Ile His Leu Tyr Gln Thr Phe  
                   115                                  120                                  125  
 Val Val Gln Leu Gln Asp Pro Arg Glu Pro Arg Arg Gln Ala Thr Gln  
                   130                                  135                                  140  
 Met Leu Lys Leu Gln Asn Leu Val Ile Pro Trp Ala Pro Glu Asn Leu  
 145                                  150                                  155                                  160  
 Thr Leu His Lys Leu Ser Glu Ser Gln Leu Glu Leu Asn Trp Asn Asn  
                   165                                  170                                  175

Arg Phe Leu Asn His Cys Leu Glu His Leu Val Gln Tyr Arg Thr Asp  
 180 185 190  
 Trp Asp His Ser Trp Thr Glu Gln Ser Val Asp Tyr Arg His Lys Phe  
 195 200 205  
 Ser Leu Pro Ser Val Asp Gly Gln Lys Arg Tyr Thr Phe Arg Val Arg  
 210 215 220  
 Ser Arg Phe Asn Pro Leu Cys Gly Ser Ala Gln His Trp Ser Glu Trp  
 225 230 235 240  
 Ser His Pro Ile His Trp Gly Ser Asn Thr Ser Lys Glu Asn Thr Val  
 245 250 255  
 Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys  
 260 265 270  
 Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg  
 275 280 285  
 Glu Ala Lys Val Gln Trp Lys Val Asp Asn Ala Leu Gln Ser Gly Asn  
 290 295 300  
 Ser Gln Glu Ser Val Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr Ser  
 305 310 315 320  
 Leu Ser Ser Thr Leu Thr Leu Ser Lys Ala Asp Tyr Glu Lys His Lys  
 325 330 335  
 Val Tyr Ala Cys Glu Val Thr His Gln Gly Leu Ser Ser Pro Val Thr  
 340 345 350  
 Lys Ser Phe Asn Arg Gly Glu Cys  
 355 360

<210> 19  
 <211> 36  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC19905

<400> 19  
 acaggatccg tcagcatgcc gcgtggctgg gccgcc

36

<210> 20  
 <211> 33  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Oligonucleotide primer ZC19906

<400> 20  
acagaattct tagctggcct ggggtccagg cgt 33

<210> 21  
<211> 36  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Oligonucleotide primer ZC19931

<400> 21  
ggttggtacc gcaagatgcc gcgtggctgg gccgcc 36

<210> 22  
<211> 29  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Oligonucleotide primer ZC19932

<400> 22  
cggaggatcc gtgaggggttc cagccttcc 29

<210> 23  
<211> 8  
<212> PRT  
<213> Artificial Sequence  
  
<220>  
<223> FLAG tag amino acid sequence

<400> 23  
Asp Tyr Lys Asp Asp Asp Asp Lys  
1 5

<210> 24  
<211> 66  
<212> DNA  
<213> Artificial Sequence

&lt;220&gt;

<223> Oligonucleotide primer spanning vector flanking  
region and the 5' end of the zalphall

&lt;400&gt; 24

tccactttgc ctttctctcc acaggtgtcc aggggaattca tcgataatgc cgcgtggctg	60
ggccgc	66

&lt;210&gt; 25

&lt;211&gt; 699

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 25

gagcccagat cttcagacaa aactcacaca tgcccaccgt gcccagcacc tgaagccgag	60
ggggcaccgt cagtcttcct cttcccccca aaacccaagg acaccctcat gatctcccgg	120
acccttgagg tcacatgcgt ggtggtggac gtgagccacg aagaccctga ggtcaagttc	180
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag	240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat	300
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc catcctccat cgagaaaacc	360
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg	420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatcccagc	480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct	540
cccgtgctgg actccgacgg ctccttcttc ctctacagca agctcaccgt ggacaagagc	600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac	660
tacacgcaga agagcctctc cctgtctccg ggtaaataa	699

&lt;210&gt; 26

&lt;211&gt; 62

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> First Oligonucleotide primer spanning 3' end of  
the zalphall extracellular domain and the 5' end  
of Fc4

&lt;400&gt; 26

gcacggtggg catgtgtgag ttttgtctga agatctgggc tcgtgagggt tccagccttc	60
ct	62

&lt;210&gt; 27

&lt;211&gt; 61



<212> DNA

<213> Artificial Sequence

<220>

<223> Second Oligonucleotide primer spanning 3' end of the zalpha11 extracellular domain and the 5' end of Fc4

<400> 27

agaccagtc agaggagtta aaggaaggct ggaaccctca cgagcccaga tcttcagaca	60
a	61

<210> 28

<211> 67

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer spanning the 3' end of Fc4 and the vector flanking region

<400> 28

gtgggcctct ggggtgggta caaccccaga gctgttttaa tctagattat ttacccggag	60
acaggga	67

<210> 29

<211> 1821

<212> DNA

<213> Artificial Sequence

<220>

<223> Polynucleotide encoding MBP-human zalpha11 soluble receptor fusion

<221> CDS

<222> (1)...(1821)

<400> 29

atg aaa atc gaa gaa ggt aaa ctg gta atc tgg att aac ggc gat aaa	48
Met Lys Ile Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp Lys	
1                      5                      10                      15	

ggc tat aac ggt ctc gct gaa gtc ggt aag aaa ttc gag aaa gat acc Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr 20 25 30	96
gga att aaa gtc acc gtt gag cat ccg gat aaa ctg gaa gag aaa ttc Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe 35 40 45	144
cca cag gtt gcg gca act ggc gat ggc cct gac att atc ttc tgg gca Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala 50 55 60	192
cac gac cgc ttt ggt ggc tac gct caa tct ggc ctg ttg gct gaa atc His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile 65 70 75 80	240
acc ccg gac aaa gcg ttc cag gac aag ctg tat ccg ttt acc tgg gat Thr Pro Asp Lys Ala Phe Gln Asp Lys Leu Tyr Pro Phe Thr Trp Asp 85 90 95	288
gcc gta cgt tac aac ggc aag ctg att gct tac ccg atc gct gtt gaa Ala Val Arg Tyr Asn Gly Lys Leu Ile Ala Tyr Pro Ile Ala Val Glu 100 105 110	336
gcg tta tcg ctg att tat aac aaa gat ctg ctg ccg aac ccg cca aaa Ala Leu Ser Leu Ile Tyr Asn Lys Asp Leu Leu Pro Asn Pro Pro Lys 115 120 125	384
acc tgg gaa gag atc ccg gcg ctg gat aaa gaa ctg aaa gcg aaa ggt Thr Trp Glu Glu Ile Pro Ala Leu Asp Lys Glu Leu Lys Ala Lys Gly 130 135 140	432
aag agc gcg ctg atg ttc aac ctg caa gaa ccg tac ttc acc tgg ccg Lys Ser Ala Leu Met Phe Asn Leu Gln Glu Pro Tyr Phe Thr Trp Pro 145 150 155 160	480
ctg att gct gct gac ggg ggt tat gcg ttc aag tat gaa aac ggc aag Leu Ile Ala Ala Asp Gly Gly Tyr Ala Phe Lys Tyr Glu Asn Gly Lys 165 170 175	528
tac gac att aaa gac gtg ggc gtg gat aac gct ggc gcg aaa gcg ggt Tyr Asp Ile Lys Asp Val Gly Val Asp Asn Ala Gly Ala Lys Ala Gly 180 185 190	576

ctg acc ttc ctg gtt gac ctg att aaa aac aaa cac atg aat gca gac Leu Thr Phe Leu Val Asp Leu Ile Lys Asn Lys His Met Asn Ala Asp 195 200 205	624
acc gat tac tcc atc gca gaa gct gcc ttt aat aaa ggc gaa aca gcg Thr Asp Tyr Ser Ile Ala Glu Ala Ala Phe Asn Lys Gly Glu Thr Ala 210 215 220	672
atg acc atc aac ggc ccg tgg gca tgg tcc aac atc gac acc agc aaa Met Thr Ile Asn Gly Pro Trp Ala Trp Ser Asn Ile Asp Thr Ser Lys 225 230 235 240	720
gtg aat tat ggt gta acg gta ctg ccg acc ttc aag ggt caa cca tcc Val Asn Tyr Gly Val Thr Val Leu Pro Thr Phe Lys Gly Gln Pro Ser 245 250 255	768
aaa ccg ttc gtt ggc gtg ctg agc gca ggt att aac gcc gcc agt ccg Lys Pro Phe Val Gly Val Leu Ser Ala Gly Ile Asn Ala Ala Ser Pro 260 265 270	816
aac aaa gag ctg gca aaa gag ttc ctc gaa aac tat ctg ctg act gat Asn Lys Glu Leu Ala Lys Glu Phe Leu Glu Asn Tyr Leu Leu Thr Asp 275 280 285	864
gaa ggt ctg gaa gcg gtt aat aaa gac aaa ccg ctg ggt gcc gta gcg Glu Gly Leu Glu Ala Val Asn Lys Asp Lys Pro Leu Gly Ala Val Ala 290 295 300	912
ctg aag tct tac gag gaa gag ttg gcg aaa gat cca cgt att gcc gcc Leu Lys Ser Tyr Glu Glu Glu Leu Ala Lys Asp Pro Arg Ile Ala Ala 305 310 315 320	960
acc atg gaa aac gcc cag aaa ggt gaa atc atg ccg aac atc ccg cag Thr Met Glu Asn Ala Gln Lys Gly Glu Ile Met Pro Asn Ile Pro Gln 325 330 335	1008
atg tcc gct ttc tgg tat gcc gtg cgt act gcg gtg atc aac gcc gcc Met Ser Ala Phe Trp Tyr Ala Val Arg Thr Ala Val Ile Asn Ala Ala 340 345 350	1056

agc ggt cgt cag act gtc gat gaa gcc ctg aaa gac gcg cag act aat Ser Gly Arg Gln Thr Val Asp Glu Ala Leu Lys Asp Ala Gln Thr Asn 355 360 365	1104
tcg agc tcc cac cat cac cat cac cac gcg aat tcg gta ccg ctg gtt Ser Ser Ser His His His His His His Ala Asn Ser Val Pro Leu Val 370 375 380	1152
ccg cgt gga tcc tgc ccc gac ctc gtc tgc tac acc gat tac ctc cag Pro Arg Gly Ser Cys Pro Asp Leu Val Cys Tyr Thr Asp Tyr Leu Gln 385 390 395 400	1200
acg gtc atc tgc atc ctg gaa atg tgg aac ctc cac ccc agc acg ctc Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu His Pro Ser Thr Leu 405 410 415	1248
acc ctt acc tgg caa gac cag tat gaa gag ctg aag gac gag gcc acc Thr Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr 420 425 430	1296
tcc tgc agc ctc cac agg tcg gcc cac aat gcc acg cat gcc acc tac Ser Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr 435 440 445	1344
acc tgc cac atg gat gta ttc cac ttc atg gcc gac gac att ttc agt Thr Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser 450 455 460	1392
gtc aac atc aca gac cag tct ggc aac tac tcc cag gag tgt ggc agc Val Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser 465 470 475 480	1440
ttt ctc ctg gct gag agc atc aag ccg gct ccc cct ttc aac gtg act Phe Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr 485 490 495	1488
gtg acc ttc tca gga cag tat aat atc tcc tgg cgc tca gat tac gaa Val Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu 500 505 510	1536
gac cct gcc ttc tac atg ctg aag ggc aag ctt cag tat gag ctg cag Asp Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln 515 520 525	1584

tac agg aac cgg gga gac ccc tgg gct gtg agt ccg agg aga aag ctg	1632
Tyr Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu	
530 535 540	
atc tca gtg gac tca aga agt gtc tcc ctc ctc ccc ctg gag ttc cgc	1680
Ile Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg	
545 550 555 560	
aaa gac tcg agc tat gag ctg cag gtg cgg gca ggg ccc atg cct ggc	1728
Lys Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly	
565 570 575	
tcc tcc tac cag ggg acc tgg agt gaa tgg agt gac ccg gtc atc ttt	1776
Ser Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe	
580 585 590	
cag acc cag tca gag gag tta aag gaa ggc tgg aac cct cac tag	1821
Gln Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His *	
595 600 605	

&lt;210&gt; 30

&lt;211&gt; 606

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> MBP-human zalphall soluble receptor fusion  
polypeptide

&lt;400&gt; 30

Met Lys Ile Glu Glu Gly Lys Leu Val Ile Trp Ile Asn Gly Asp Lys	
1 5 10 15	
Gly Tyr Asn Gly Leu Ala Glu Val Gly Lys Lys Phe Glu Lys Asp Thr	
20 25 30	
Gly Ile Lys Val Thr Val Glu His Pro Asp Lys Leu Glu Glu Lys Phe	
35 40 45	
Pro Gln Val Ala Ala Thr Gly Asp Gly Pro Asp Ile Ile Phe Trp Ala	
50 55 60	
His Asp Arg Phe Gly Gly Tyr Ala Gln Ser Gly Leu Leu Ala Glu Ile	
65 70 75 80	

Thr	Pro	Asp	Lys	Ala	Phe	Gln	Asp	Lys	Leu	Tyr	Pro	Phe	Thr	Trp	Asp		
				85					90					95			
Ala	Val	Arg	Tyr	Asn	Gly	Lys	Leu	Ile	Ala	Tyr	Pro	Ile	Ala	Val	Glu		
			100					105					110				
Ala	Leu	Ser	Leu	Ile	Tyr	Asn	Lys	Asp	Leu	Leu	Pro	Asn	Pro	Pro	Lys		
		115					120					125					
Thr	Trp	Glu	Glu	Ile	Pro	Ala	Leu	Asp	Lys	Glu	Leu	Lys	Ala	Lys	Gly		
	130					135					140						
Lys	Ser	Ala	Leu	Met	Phe	Asn	Leu	Gln	Glu	Pro	Tyr	Phe	Thr	Trp	Pro		
145					150					155					160		
Leu	Ile	Ala	Ala	Asp	Gly	Gly	Tyr	Ala	Phe	Lys	Tyr	Glu	Asn	Gly	Lys		
				165					170					175			
Tyr	Asp	Ile	Lys	Asp	Val	Gly	Val	Asp	Asn	Ala	Gly	Ala	Lys	Ala	Gly		
		180						185					190				
Leu	Thr	Phe	Leu	Val	Asp	Leu	Ile	Lys	Asn	Lys	His	Met	Asn	Ala	Asp		
	195					200						205					
Thr	Asp	Tyr	Ser	Ile	Ala	Glu	Ala	Ala	Phe	Asn	Lys	Gly	Glu	Thr	Ala		
	210				215						220						
Met	Thr	Ile	Asn	Gly	Pro	Trp	Ala	Trp	Ser	Asn	Ile	Asp	Thr	Ser	Lys		
225					230					235					240		
Val	Asn	Tyr	Gly	Val	Thr	Val	Leu	Pro	Thr	Phe	Lys	Gly	Gln	Pro	Ser		
			245					250						255			
Lys	Pro	Phe	Val	Gly	Val	Leu	Ser	Ala	Gly	Ile	Asn	Ala	Ala	Ser	Pro		
		260						265					270				
Asn	Lys	Glu	Leu	Ala	Lys	Glu	Phe	Leu	Glu	Asn	Tyr	Leu	Leu	Thr	Asp		
	275					280						285					
Glu	Gly	Leu	Glu	Ala	Val	Asn	Lys	Asp	Lys	Pro	Leu	Gly	Ala	Val	Ala		
	290					295				300							
Leu	Lys	Ser	Tyr	Glu	Glu	Glu	Leu	Ala	Lys	Asp	Pro	Arg	Ile	Ala	Ala		
305					310					315					320		
Thr	Met	Glu	Asn	Ala	Gln	Lys	Gly	Glu	Ile	Met	Pro	Asn	Ile	Pro	Gln		
			325					330						335			
Met	Ser	Ala	Phe	Trp	Tyr	Ala	Val	Arg	Thr	Ala	Val	Ile	Asn	Ala	Ala		
		340				345						350					
Ser	Gly	Arg	Gln	Thr	Val	Asp	Glu	Ala	Leu	Lys	Asp	Ala	Gln	Thr	Asn		
		355				360						365					
Ser	Ser	Ser	His	His	His	His	His	His	Ala	Asn	Ser	Val	Pro	Leu	Val		
	370					375					380						
Pro	Arg	Gly	Ser	Cys	Pro	Asp	Leu	Val	Cys	Tyr	Thr	Asp	Tyr	Leu	Gln		
385					390					395					400		
Thr	Val	Ile	Cys	Ile	Leu	Glu	Met	Trp	Asn	Leu	His	Pro	Ser	Thr	Leu		
			405					410						415			

Thr Leu Thr Trp Gln Asp Gln Tyr Glu Glu Leu Lys Asp Glu Ala Thr  
                   420                  425                  430  
 Ser Cys Ser Leu His Arg Ser Ala His Asn Ala Thr His Ala Thr Tyr  
           435                  440                  445  
 Thr Cys His Met Asp Val Phe His Phe Met Ala Asp Asp Ile Phe Ser  
       450                  455                  460  
 Val Asn Ile Thr Asp Gln Ser Gly Asn Tyr Ser Gln Glu Cys Gly Ser  
 465                  470                  475                  480  
 Phe Leu Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Phe Asn Val Thr  
                   485                  490                  495  
 Val Thr Phe Ser Gly Gln Tyr Asn Ile Ser Trp Arg Ser Asp Tyr Glu  
           500                  505                  510  
 Asp Pro Ala Phe Tyr Met Leu Lys Gly Lys Leu Gln Tyr Glu Leu Gln  
       515                  520                  525  
 Tyr Arg Asn Arg Gly Asp Pro Trp Ala Val Ser Pro Arg Arg Lys Leu  
       530                  535                  540  
 Ile Ser Val Asp Ser Arg Ser Val Ser Leu Leu Pro Leu Glu Phe Arg  
 545                  550                  555                  560  
 Lys Asp Ser Ser Tyr Glu Leu Gln Val Arg Ala Gly Pro Met Pro Gly  
                   565                  570                  575  
 Ser Ser Tyr Gln Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe  
           580                  585                  590  
 Gln Thr Gln Ser Glu Glu Leu Lys Glu Gly Trp Asn Pro His  
       595                  600                  605

&lt;210&gt; 31

&lt;211&gt; 657

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 31

tgccccgacc	tcgtctgcta	caccgattac	ctccagacgg	tcattctgcat	cctggaaatg	60
tggaacctcc	accccagcac	gctcaccctt	acctggcaag	accagtatga	agagctgaag	120
gacgaggcca	cctcctgcag	cctccacagg	tcggcccaca	atgccacgca	tgccacctac	180
acctgccaca	tggaatgtatt	ccacttcatg	gccgacgaca	ttttcagtgt	caacatcaca	240
gaccagtctg	gcaactactc	ccaggagtgt	ggcagctttc	tcctggctga	gagcatcaag	300
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Glu His Ala Ala Phe Ala Cys Phe Gln Lys Ala Lys Leu Lys Pro Ser
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Met	Trp	Asn	Leu	His	Pro	Ser	Thr	Leu	Thr	Leu	Thr	Trp	Ile	Leu	Ser
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Asn	Asn	Thr	Gly	Cys	Tyr	Ile	Lys	Asp	Arg	Thr	Leu	Asp	Leu	Arg	Gln
				85					90					95	
Asp	Gln	Tyr	Glu	Glu	Leu	Lys	Asp	Glu	Ala	Thr	Ser	Cys	Ser	Leu	His
			100					105					110		
Arg	Ser	Ala	His	Asn	Ala	Thr	His	Ala	Thr	Tyr	Thr	Cys	His	Met	Asp
		115					120					125			
Val	Phe	His	Phe	Met	Ala	Asp	Asp	Ile	Phe	Ser	Val	Asn	Ile	Thr	Asp
	130					135					140				

Gln	Ser	Gly	Asn	Tyr	Ser	Gln	Glu	Cys	Gly	Ser	Phe	Leu	Leu	Ala	Glu
145					150					155					160
Ser	Arg	Gln	Tyr	Asn	Ile	Ser	Trp	Arg	Ser	Asp	Tyr	Glu	Asp	Pro	Ala
				165					170					175	
Phe	Tyr	Met	Leu	Lys	Gly	Lys	Leu	Gln	Tyr	Glu	Leu	Gln	Tyr	Arg	Asn
			180					185					190		
Arg	Gly	Asp	Pro	Trp	Ala	Val	Ser	Pro	Arg	Arg	Lys	Leu	Ile	Ser	Val
		195					200					205			
Asp	Ser	Arg	Ser	Val	Ser	Leu	Leu	Pro	Leu	Glu	Phe	Arg	Lys	Asp	Ser
	210					215					220				
Ser	Tyr	Glu	Leu	Gln	Val	Arg	Ala	Gly	Pro	Met	Pro	Gly	Ser	Ser	Tyr
225					230					235					240
Gln	Gly	Thr	Trp	Ser	Glu	Trp	Ser	Asp	Pro	Val	Ile	Phe	Gln	Thr	Gln
				245					250					255	
Ser	Glu	Glu	Leu	Lys	Glu	Gly	Trp	Asn	Pro	His	Leu	Leu	Leu	Leu	Leu
			260					265					270		
Leu	Leu	Val	Ile	Val	Phe	Ile	Pro	Ala	Phe	Trp	Ser	Leu	Lys	Thr	His
		275					280					285			
Pro	Leu	Trp	Arg	Leu	Trp	Lys	Lys	Ile	Trp	Ala	Val	Pro	Ser	Pro	Glu
	290					295					300				
Arg	Phe	Phe	Met	Pro	Leu	Tyr	Lys	Gly	Cys	Ser	Gly	Asp	Phe	Lys	Lys
305					310					315					320
Trp	Val	Gly	Ala	Pro	Phe	Thr	Gly	Ser	Ser	Leu	Glu	Leu	Gly	Pro	Trp
				325					330					335	
Ser	Pro	Glu	Val	Pro	Ser	Thr	Leu	Glu	Val	Tyr	Ser	Cys	His	Pro	Pro
			340					345					350		
Arg	Ser	Pro	Ala	Lys	Arg	Leu	Gln	Leu	Thr	Glu	Leu	Gln	Glu	Pro	Ala
		355					360					365			
Glu	Leu	Val	Glu	Ser	Asp	Gly	Val	Pro	Lys	Pro	Ser	Phe	Trp	Pro	Thr
	370					375					380				
Ala	Gln	Asn	Ser	Gly	Gly	Ser	Ala	Tyr	Ser	Glu	Glu	Arg	Asp	Arg	Pro
385					390					395					400
Tyr	Gly	Leu	Val	Ser	Ile	Asp	Thr	Val	Thr	Val	Leu	Asp	Ala	Glu	Gly
				405					410					415	
Pro	Cys	Thr	Trp	Pro	Cys	Ser	Cys	Glu	Asp	Asp	Gly	Tyr	Pro	Ala	Leu
			420					425					430		
Asp	Leu	Asp	Ala	Gly	Leu	Glu	Pro	Ser	Pro	Gly	Leu	Glu	Asp	Pro	Leu
		435					440					445			
Leu	Asp	Ala	Gly	Thr	Thr	Val	Leu	Ser	Cys	Gly	Cys	Val	Ser	Ala	Gly
	450					455					460				
Ser	Pro	Gly	Leu	Gly	Gly	Pro	Leu	Gly	Ser	Leu	Leu	Asp	Arg	Leu	Lys
465					470					475					480

[illegible]

<210> 66  
<211> 741  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Degenerate polynucleotide sequence of SEQ ID NO:69

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<221> misc_feature
<222> (1)...(741)
<223> n = A,T,C or G
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<400>	66					
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ccnccnggnt	gggngtgycc	ngayytngtn	tgytayacng	aytayytnc	racngtnath	120
tgyathytn	aratgtggaa	yytncaayccn	wsnacnytna	cnytnacntg	gathytnwsn	180
aayaayacng	gntgytayat	haargaymgn	acnytngayy	tnmgncarga	ycartaygar	240
garytnaarg	aygargcnac	nwsntgywsn	ytncaymgw	sngcncayaa	ygcnacncay	300
gcnacntaya	cntgycayat	ggaygtntty	cayttyatgg	cngaygayat	httywsngtn	360
aayathacng	aycarwsngg	naaytaywsn	cargartgyg	gnwsnttyyt	nytngcngar	420
wsnmgncart	ayaayathws	ntggmgwnsn	gaytaygarg	ayccngcntt	ytayatgytn	480
aarggnaary	tncartayga	rytncartay	mgnaaymgng	gngayccntg	ggcngtnwsn	540
ccnmgmgna	arytnathws	ngtngaywsn	mgwnsngtnw	snytynytncc	nytngartty	600
mgnaargayw	snwsntayga	rytncargtn	mgngcnggnc	cnatgccngg	nwsnwsntay	660
carggnacnt	ggwsngartg	gwsngayccn	gtnathhttyc	aracncarws	ngargarytn	720
aargarggnt	ggaayccnca	y				741

<210> 67  
<211> 4  
<212> PRT



<213> Artificial Sequence

<220>

<223> WXXW motif

<221> VARIANT

<222> (1)...(4)

<223> Xaa = Any Amino Acid

<400> 67

Trp Xaa Xaa Trp

1

<210> 68

<211> 741

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)...(741)

<400> 68

atg	gag	agg	aag	ctc	tgc	agt	ccc	aag	cca	ccc	ccc	acc	aag	gcc	tct	48
Met	Glu	Arg	Lys	Leu	Cys	Ser	Pro	Lys	Pro	Pro	Pro	Thr	Lys	Ala	Ser	
1				5				10					15			

ctc	ccc	act	gac	cct	cca	ggc	tgg	ggc	tgc	ccc	gac	ctc	gtc	tgc	tac	96
Leu	Pro	Thr	Asp	Pro	Pro	Gly	Trp	Gly	Cys	Pro	Asp	Leu	Val	Cys	Tyr	
			20				25						30			

acc	gat	tac	ctc	cag	acg	gtc	atc	tgc	atc	ctg	gaa	atg	tgg	aac	ctc	144
Thr	Asp	Tyr	Leu	Gln	Thr	Val	Ile	Cys	Ile	Leu	Glu	Met	Trp	Asn	Leu	
			35				40					45				

cac	ccc	agc	acg	ctc	acc	ctt	acc	tgg	ata	ctt	tct	aat	aat	act	ggg	192
His	Pro	Ser	Thr	Leu	Thr	Leu	Thr	Trp	Ile	Leu	Ser	Asn	Asn	Thr	Gly	
			50				55				60					

tgc	tat	atc	aag	gac	aga	aca	ctg	gac	ctc	agg	caa	gac	cag	tat	gaa	240
Cys	Tyr	Ile	Lys	Asp	Arg	Thr	Leu	Asp	Leu	Arg	Gln	Asp	Gln	Tyr	Glu	
65						70				75					80	

gag ctg aag gac gag gcc acc tcc tgc agc ctc cac agg tcg gcc cac Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu His Arg Ser Ala His 85 90 95	288
aat gcc acg cat gcc acc tac acc tgc cac atg gat gta ttc cac ttc Asn Ala Thr His Ala Thr Tyr Thr Cys His Met Asp Val Phe His Phe 100 105 110	336
atg gcc gac gac att ttc agt gtc aac atc aca gac cag tct ggc aac Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr Asp Gln Ser Gly Asn 115 120 125	384
tac tcc cag gag tgt ggc agc ttt ctc ctg gct gag agc aga cag tat Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala Glu Ser Arg Gln Tyr 130 135 140	432
aat atc tcc tgg cgc tca gat tac gaa gac cct gcc ttc tac atg ctg Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala Phe Tyr Met Leu 145 150 155 160	480
aag ggc aag ctt cag tat gag ctg cag tac agg aac cgg gga gac ccc Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Arg Gly Asp Pro 165 170 175	528
tgg gct gtg agt ccg agg aga aag ctg atc tca gtg gac tca aga agt Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val Asp Ser Arg Ser 180 185 190	576
gtc tcc ctc ctc ccc ctg gag ttc cgc aaa gac tcg agc tat gag ctg Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser Tyr Glu Leu 195 200 205	624
cag gtg cgg gca ggg ccc atg cct ggc tcc tcc tac cag ggg acc tgg Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln Gly Thr Trp 210 215 220	672
agt gaa tgg agt gac ccg gtc atc ttt cag acc cag tca gag gag tta Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser Glu Glu Leu 225 230 235 240	720
aag gaa ggc tgg aac cct cac Lys Glu Gly Trp Asn Pro His 245	741

<210> 69  
 <211> 247  
 <212> PRT  
 <213> Homo sapiens

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 Leu Pro Thr Asp Pro Pro Gly Trp Gly Cys Pro Asp Leu Val Cys Tyr  
 20 25 30  
 Thr Asp Tyr Leu Gln Thr Val Ile Cys Ile Leu Glu Met Trp Asn Leu  
 35 40 45  
 His Pro Ser Thr Leu Thr Leu Thr Trp Ile Leu Ser Asn Asn Thr Gly  
 50 55 60  
 Cys Tyr Ile Lys Asp Arg Thr Leu Asp Leu Arg Gln Asp Gln Tyr Glu  
 65 70 75 80  
 Glu Leu Lys Asp Glu Ala Thr Ser Cys Ser Leu His Arg Ser Ala His  
 85 90 95  
 Asn Ala Thr His Ala Thr Tyr Thr Cys His Met Asp Val Phe His Phe  
 100 105 110  
 Met Ala Asp Asp Ile Phe Ser Val Asn Ile Thr Asp Gln Ser Gly Asn  
 115 120 125  
 Tyr Ser Gln Glu Cys Gly Ser Phe Leu Leu Ala Glu Ser Arg Gln Tyr  
 130 135 140  
 Asn Ile Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala Phe Tyr Met Leu  
 145 150 155 160  
 Lys Gly Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Arg Gly Asp Pro  
 165 170 175  
 Trp Ala Val Ser Pro Arg Arg Lys Leu Ile Ser Val Asp Ser Arg Ser  
 180 185 190  
 Val Ser Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser Tyr Glu Leu  
 195 200 205  
 Gln Val Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln Gly Thr Trp  
 210 215 220  
 Ser Glu Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser Glu Glu Leu  
 225 230 235 240  
 Lys Glu Gly Trp Asn Pro His  
 245

<210> 70  
 <211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Domain linker motif; PAPP motif

<400> 70

Pro Ala Pro Pro

1

<210> 71

<211> 261

<212> PRT

<213> Artificial Sequence

<220>

<223> Representative variant soluble receptor with domain linker

<221> VARIANT

<222> (1)...(261)

<223> Xaa = Any Amino Acid

<400> 71

Met	Glu	Arg	Lys	Leu	Cys	Ser	Pro	Lys	Pro	Pro	Pro	Thr	Lys	Ala	Ser
1			5					10						15	
Leu	Pro	Thr	Asp	Pro	Pro	Gly	Trp	Gly	Cys	Pro	Asp	Leu	Val	Cys	Tyr
			20					25					30		
Thr	Asp	Tyr	Leu	Gln	Thr	Val	Ile	Cys	Ile	Leu	Glu	Met	Trp	Asn	Leu
		35					40					45			
His	Pro	Ser	Thr	Leu	Thr	Leu	Thr	Trp	Ile	Leu	Ser	Asn	Asn	Thr	Gly
	50				55					60					
Cys	Tyr	Ile	Lys	Asp	Arg	Thr	Leu	Asp	Leu	Arg	Gln	Asp	Gln	Tyr	Glu
65				70				75						80	
Glu	Leu	Lys	Asp	Glu	Ala	Thr	Ser	Cys	Ser	Leu	His	Arg	Ser	Ala	His
			85					90						95	
Asn	Ala	Thr	His	Ala	Thr	Tyr	Thr	Cys	His	Met	Asp	Val	Phe	His	Phe
		100						105					110		
Met	Ala	Asp	Asp	Ile	Phe	Ser	Val	Asn	Ile	Thr	Asp	Gln	Ser	Gly	Asn
	115					120					125				
Tyr	Ser	Gln	Glu	Cys	Gly	Ser	Phe	Leu	Leu	Ala	Glu	Ser	Xaa	Xaa	Pro
	130					135					140				

Ala Pro Pro Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Arg Gln Tyr Asn Ile  
 145 150 155 160  
 Ser Trp Arg Ser Asp Tyr Glu Asp Pro Ala Phe Tyr Met Leu Lys Gly  
 165 170 175  
 Lys Leu Gln Tyr Glu Leu Gln Tyr Arg Asn Arg Gly Asp Pro Trp Ala  
 180 185 190  
 Val Ser Pro Arg Arg Lys Leu Ile Ser Val Asp Ser Arg Ser Val Ser  
 195 200 205  
 Leu Leu Pro Leu Glu Phe Arg Lys Asp Ser Ser Tyr Glu Leu Gln Val  
 210 215 220  
 Arg Ala Gly Pro Met Pro Gly Ser Ser Tyr Gln Gly Thr Trp Ser Glu  
 225 230 235 240  
 Trp Ser Asp Pro Val Ile Phe Gln Thr Gln Ser Glu Glu Leu Lys Glu  
 245 250 255  
 Gly Trp Asn Pro His  
 260

<210> 72

<211> 1461

<212> DNA

<213> Artificial Sequence

<220>

<223> Mouse zalphall extracellular domain murine  
 immunoglobulin gamma 2a heavy chain Fc region  
 fusion protein (zalphallm-mG2a) Polynucleotide

<221> CDS

<222> (1)...(1461)

<400> 72

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gcc gtc ttc gtt tcg ctc agc cag aaa atc cat gcc gag ttg aga cgc	96
Ala Val Phe Val Ser Leu Ser Gln Lys Ile His Ala Glu Leu Arg Arg	
20 25 30	
ttc cgg aga tgc ctg gac ctc act tgc tac act gac tac ctc tgg acc	144
Phe Arg Arg Cys Leu Asp Leu Thr Cys Tyr Thr Asp Tyr Leu Trp Thr	
35 40 45	

atc acc tgt gtc ctg gag aca cgg agc ccc aac ccc agc ata ctc agt Ile Thr Cys Val Leu Glu Thr Arg Ser Pro Asn Pro Ser Ile Leu Ser 50 55 60	192
ctc acc tgg caa gat gaa tat gag gaa ctt cag gac caa gag acc ttc Leu Thr Trp Gln Asp Glu Tyr Glu Glu Leu Gln Asp Gln Glu Thr Phe 65 70 75 80	240
tgc agc cta cac agg tct ggc cac aac acc aca cat ata tgg tac acg Cys Ser Leu His Arg Ser Gly His Asn Thr Thr His Ile Trp Tyr Thr 85 90 95	288
tgc cat atg cgc ttg tct caa ttc ctg tcc gat gaa gtt ttc att gtc Cys His Met Arg Leu Ser Gln Phe Leu Ser Asp Glu Val Phe Ile Val 100 105 110	336
aat gtg acg gac cag tct ggc aac aac tcc caa gag tgt ggc agc ttt Asn Val Thr Asp Gln Ser Gly Asn Asn Ser Gln Glu Cys Gly Ser Phe 115 120 125	384
gtc ctg gct gag agc atc aaa cca gct ccc ccc ttg aac gtg act gtg Val Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Leu Asn Val Thr Val 130 135 140	432
gcc ttc tca gga cgc tat gat atc tcc tgg gac tca gct tat gac gaa Ala Phe Ser Gly Arg Tyr Asp Ile Ser Trp Asp Ser Ala Tyr Asp Glu 145 150 155 160	480
ccc tcc aac tac gtg ctg agg ggc aag cta caa tat gag ctg cag tat Pro Ser Asn Tyr Val Leu Arg Gly Lys Leu Gln Tyr Glu Leu Gln Tyr 165 170 175	528
cgg aac ctc aga gac ccc tat gct gtg agg ccg gtg acc aag ctg atc Arg Asn Leu Arg Asp Pro Tyr Ala Val Arg Pro Val Thr Lys Leu Ile 180 185 190	576
tca gtg gac tca aga aac gtc tct ctt ctc cct gaa gag ttc cac aaa Ser Val Asp Ser Arg Asn Val Ser Leu Leu Pro Glu Glu Phe His Lys 195 200 205	624
gat tct agc tac cag ctg cag gtg cgg gca gcg cct cag cca ggc act Asp Ser Ser Tyr Gln Leu Gln Val Arg Ala Ala Pro Gln Pro Gly Thr 210 215 220	672

tca ttc agg ggg acc tgg agt gag tgg agt gac ccc gtc atc ttt cag	720
Ser Phe Arg Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln	
225 230 235 240	
acc cag gct ggg gag ccc gag gca ggc tgg gac cct cac gag ccc aga	768
Thr Gln Ala Gly Glu Pro Glu Ala Gly Trp Asp Pro His Glu Pro Arg	
245 250 255	
tct ccc aca atc aag ccc tgt cct cca tgc aaa tgc cca gca cct aac	816
Ser Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn	
260 265 270	
ctc ttg ggt gga cca tcc gtc ttc atc ttc cct cca aag atc aag gat	864
Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp	
275 280 285	
gta ctc atg atc tcc ctg agc ccc ata gtc aca tgt gtg gtg gtg gat	912
Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp	
290 295 300	
gtg agc gag gat gac cca gat gtc cag atc agc tgg ttt gtg aac aac	960
Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn	
305 310 315 320	
gtg gaa gta cac aca gct cag aca caa acc cat aga gag gat tac aac	1008
Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn	
325 330 335	
agt act ctc cgg gtg gtc agt gcc ctc ccc atc cag cac cag gac tgg	1056
Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp	
340 345 350	
atg agt ggc aag gag ttc aaa tgc aag gtc aac aac aaa gac ctc cca	1104
Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro	
355 360 365	
gcg ccc atc gag aga acc atc tca aaa ccc aaa ggg tca gta aga gct	1152
Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala	
370 375 380	

cca	cag	gta	tat	gtc	ttg	cct	cca	cca	gaa	gaa	gag	atg	act	aag	aaa	1200
Pro	Gln	Val	Tyr	Val	Leu	Pro	Pro	Pro	Glu	Glu	Glu	Met	Thr	Lys	Lys	
385					390				395						400	

cag	gtc	act	ctg	acc	tgc	atg	gtc	aca	gac	ttc	atg	cct	gaa	gac	att	1248
Gln	Val	Thr	Leu	Thr	Cys	Met	Val	Thr	Asp	Phe	Met	Pro	Glu	Asp	Ile	
			405						410						415	

tac	gtg	gag	tgg	acc	aac	aac	ggg	aaa	aca	gag	cta	aac	tac	aag	aac	1296
Tyr	Val	Glu	Trp	Thr	Asn	Asn	Gly	Lys	Thr	Glu	Leu	Asn	Tyr	Lys	Asn	
			420					425						430		

act	gaa	cca	gtc	ctg	gac	tct	gat	ggg	tct	tac	ttc	atg	tac	agc	aag	1344
Thr	Glu	Pro	Val	Leu	Asp	Ser	Asp	Gly	Ser	Tyr	Phe	Met	Tyr	Ser	Lys	
		435					440					445				

ctg	aga	gtg	gaa	aag	aag	aac	tgg	gtg	gaa	aga	aat	agc	tac	tcc	tgt	1392
Leu	Arg	Val	Glu	Lys	Lys	Asn	Trp	Val	Glu	Arg	Asn	Ser	Tyr	Ser	Cys	
	450					455					460					

tca	gtg	gtc	cac	gag	ggg	ctg	cac	aat	cac	cac	acg	act	aag	agc	ttc	1440
Ser	Val	Val	His	Glu	Gly	Leu	His	Asn	His	His	Thr	Thr	Lys	Ser	Phe	
465					470					475					480	

tcc	cgg	act	ccg	ggg	aaa	taa										1461
Ser	Arg	Thr	Pro	Gly	Lys	*										
				485												

&lt;210&gt; 73

&lt;211&gt; 486

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Mouse zalphall extracellular domain murine  
immunoglobulin gamma 2a heavy chain Fc region  
fusion protein

&lt;400&gt; 73

Met	Asp	Ala	Met	Lys	Arg	Gly	Leu	Cys	Cys	Val	Leu	Leu	Leu	Cys	Gly
1				5				10						15	



Ala Val Phe Val Ser Leu Ser Gln Lys Ile His Ala Glu Leu Arg Arg  
 20 25 30  
 Phe Arg Arg Cys Leu Asp Leu Thr Cys Tyr Thr Asp Tyr Leu Trp Thr  
 35 40 45  
 Ile Thr Cys Val Leu Glu Thr Arg Ser Pro Asn Pro Ser Ile Leu Ser  
 50 55 60  
 Leu Thr Trp Gln Asp Glu Tyr Glu Glu Leu Gln Asp Gln Glu Thr Phe  
 65 70 75 80  
 Cys Ser Leu His Arg Ser Gly His Asn Thr Thr His Ile Trp Tyr Thr  
 85 90 95  
 Cys His Met Arg Leu Ser Gln Phe Leu Ser Asp Glu Val Phe Ile Val  
 100 105 110  
 Asn Val Thr Asp Gln Ser Gly Asn Asn Ser Gln Glu Cys Gly Ser Phe  
 115 120 125  
 Val Leu Ala Glu Ser Ile Lys Pro Ala Pro Pro Leu Asn Val Thr Val  
 130 135 140  
 Ala Phe Ser Gly Arg Tyr Asp Ile Ser Trp Asp Ser Ala Tyr Asp Glu  
 145 150 155 160  
 Pro Ser Asn Tyr Val Leu Arg Gly Lys Leu Gln Tyr Glu Leu Gln Tyr  
 165 170 175  
 Arg Asn Leu Arg Asp Pro Tyr Ala Val Arg Pro Val Thr Lys Leu Ile  
 180 185 190  
 Ser Val Asp Ser Arg Asn Val Ser Leu Leu Pro Glu Glu Phe His Lys  
 195 200 205  
 Asp Ser Ser Tyr Gln Leu Gln Val Arg Ala Ala Pro Gln Pro Gly Thr  
 210 215 220  
 Ser Phe Arg Gly Thr Trp Ser Glu Trp Ser Asp Pro Val Ile Phe Gln  
 225 230 235 240  
 Thr Gln Ala Gly Glu Pro Glu Ala Gly Trp Asp Pro His Glu Pro Arg  
 245 250 255  
 Ser Pro Thr Ile Lys Pro Cys Pro Pro Cys Lys Cys Pro Ala Pro Asn  
 260 265 270  
 Leu Leu Gly Gly Pro Ser Val Phe Ile Phe Pro Pro Lys Ile Lys Asp  
 275 280 285  
 Val Leu Met Ile Ser Leu Ser Pro Ile Val Thr Cys Val Val Val Asp  
 290 295 300  
 Val Ser Glu Asp Asp Pro Asp Val Gln Ile Ser Trp Phe Val Asn Asn  
 305 310 315 320  
 Val Glu Val His Thr Ala Gln Thr Gln Thr His Arg Glu Asp Tyr Asn  
 325 330 335  
 Ser Thr Leu Arg Val Val Ser Ala Leu Pro Ile Gln His Gln Asp Trp  
 340 345 350

Met Ser Gly Lys Glu Phe Lys Cys Lys Val Asn Asn Lys Asp Leu Pro  
           355                          360                          365  
 Ala Pro Ile Glu Arg Thr Ile Ser Lys Pro Lys Gly Ser Val Arg Ala  
           370                          375                          380  
 Pro Gln Val Tyr Val Leu Pro Pro Pro Glu Glu Glu Met Thr Lys Lys  
 385                          390                          395                          400  
 Gln Val Thr Leu Thr Cys Met Val Thr Asp Phe Met Pro Glu Asp Ile  
                           405                          410                          415  
 Tyr Val Glu Trp Thr Asn Asn Gly Lys Thr Glu Leu Asn Tyr Lys Asn  
                           420                          425                          430  
 Thr Glu Pro Val Leu Asp Ser Asp Gly Ser Tyr Phe Met Tyr Ser Lys  
           435                          440                          445  
 Leu Arg Val Glu Lys Lys Asn Trp Val Glu Arg Asn Ser Tyr Ser Cys  
           450                          455                          460  
 Ser Val Val His Glu Gly Leu His Asn His His Thr Thr Lys Ser Phe  
 465                          470                          475                          480  
 Ser Arg Thr Pro Gly Lys  
                           485

&lt;210&gt; 74

&lt;211&gt; 23

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC26644

&lt;400&gt; 74

ggggtcgacg gccggccacc atg

23

&lt;210&gt; 75

&lt;211&gt; 35

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Oligonucleotide primer ZC26641

&lt;400&gt; 75

caagtgaggt ccaggcatct ccggaagcgt ctcaa

35

&lt;210&gt; 76

&lt;211&gt; 35

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC26642

<400> 76

ttgagacgct tccggagatg cctggacctc acttg

35

<210> 77

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC26662

<400> 77

tgtgggagat ctgggctcgt gaggggtccca gcctgc

36

<210> 78

<211> 30

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC26643

<400> 78

gagcccagat ctcccacaat caagccctgt

30

<210> 79

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Oligonucleotide primer ZC26645

<400> 79

aaacgcggcc gcggatccgg c

21

<210> 80  
 <211> 35  
 <212> PRT  
 <213> Homo sapeins

<400> 80  
 Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly  
 1 5 10 15  
 Ala Val Phe Val Ser Leu Ser Gln Glu Ile His Ala Glu Leu Arg Arg  
 20 25 30  
 Phe Arg Arg  
 35

<210> 81  
 <211> 966  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(966)

<400> 81  
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 Gly Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn  
 1 5 10 15  
 ttg agt gtc tct gtt gaa aac ctc tgc aca gta ata tgg aca tgg aat 96  
 Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn  
 20 25 30  
 cca ccc gag gga gcc agc tca aat tgt agt cta tgg tat ttt agt cat 144  
 Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp Tyr Phe Ser His  
 35 40 45  
 ttt ggc gac aaa caa gat aag aaa ata gct ccg gaa act cgt cgt tca 192  
 Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu Thr Arg Arg Ser  
 50 55 60  
 ata gaa gta ccc ctg aat gag agg att tgt ctg caa gtg ggg tcc cag 240  
 Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln Val Gly Ser Gln  
 65 70 75 80

69  
 tgt agc acc aat gag agt gag aag cct agc att ttg gtt gaa aaa tgc 288  
 Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu Val Glu Lys Cys 95  
 85  
 atc tca ccc cca gaa ggt gat cct gag tct gct gtg act gag ctt caa 336  
 Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr Glu Leu Gln 110  
 105  
 tgc att tgg cac aac ctg agc tac atg aag tgt tct tgg ctc cct gga 384  
 Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp Leu Pro Gly 125  
 120  
 agg aat acc agt ccc gac act aac tat act ctc tac tat tgg cac aga 432  
 Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr Trp His Arg 140  
 135  
 agc ctg gaa aaa att cat caa tgt gaa aac atc ttt aga gaa ggc caa 480  
 Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe Arg Glu Gly Gln 155  
 145  
 tac ttt ggt tgt tcc ttt gat ctg acc aaa gtg aag gat tcc agt ttt 528  
 Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys Asp Ser Ser Phe 170  
 165  
 gaa caa cac agt gtc caa ata atg gtc aag gat aat gca gga aaa att 576  
 Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn Ala Gly Lys Ile 185  
 180  
 aaa cca tcc ttc aat ata gtg cct tta act tcc cgt gtg aaa cct gat 624  
 Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg Val Lys Pro Asp 200  
 195  
 cct cca cat att aaa aac ctc tcc ttc cac aat gat gac cta tat gtg 672  
 Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp Asp Val Lys Tyr Val 205  
 210  
 caa tgg gag aat cca cag aat ttt att agc aga tgc cta ttt tat gaa 720  
 Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys Leu Phe Tyr Glu 220  
 225  
 gta gaa gtc aat aac agc caa act gag aca cat aat gtt ttc tac gtc 768  
 Val Glu Val Asn Ser Gln Thr Glu Thr His Asn Val Phe Tyr Val 240  
 245

caa gag gct aaa tgt gag aat cca gaa ttt gag aga aat gtg gag aat	816
Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg Asn Val Glu Asn	
260 265 270	
aca tct tgt ttc atg gtc cct ggt gtt ctt cct gat act ttg aac aca	864
Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr	
275 280 285	
gtc aga ata aga gtc aaa aca aat aag tta tgc tat gag gat gac aaa	912
Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys	
290 295 300	
ctc tgg agt aat tgg agc caa gaa atg agt ata ggt aag aag cgc aat	960
Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly Lys Lys Arg Asn	
305 310 315 320	
tcc aca	966
Ser Thr	

<210> 82  
 <211> 322  
 <212> PRT  
 <213> Homo sapiens

<400> 82	
Gly Gly Gly Gly Ala Ala Pro Thr Glu Thr Gln Pro Pro Val Thr Asn	
1 5 10 15	
Leu Ser Val Ser Val Glu Asn Leu Cys Thr Val Ile Trp Thr Trp Asn	
20 25 30	
Pro Pro Glu Gly Ala Ser Ser Asn Cys Ser Leu Trp Tyr Phe Ser His	
35 40 45	
Phe Gly Asp Lys Gln Asp Lys Lys Ile Ala Pro Glu Thr Arg Arg Ser	
50 55 60	
Ile Glu Val Pro Leu Asn Glu Arg Ile Cys Leu Gln Val Gly Ser Gln	
65 70 75 80	
Cys Ser Thr Asn Glu Ser Glu Lys Pro Ser Ile Leu Val Glu Lys Cys	
85 90 95	
Ile Ser Pro Pro Glu Gly Asp Pro Glu Ser Ala Val Thr Glu Leu Gln	
100 105 110	

Cys Ile Trp His Asn Leu Ser Tyr Met Lys Cys Ser Trp Leu Pro Gly  
           115                          120                          125  
 Arg Asn Thr Ser Pro Asp Thr Asn Tyr Thr Leu Tyr Tyr Trp His Arg  
           130                          135                          140  
 Ser Leu Glu Lys Ile His Gln Cys Glu Asn Ile Phe Arg Glu Gly Gln  
 145                          150                          155                          160  
 Tyr Phe Gly Cys Ser Phe Asp Leu Thr Lys Val Lys Asp Ser Ser Phe  
                           165                          170                          175  
 Glu Gln His Ser Val Gln Ile Met Val Lys Asp Asn Ala Gly Lys Ile  
                           180                          185                          190  
 Lys Pro Ser Phe Asn Ile Val Pro Leu Thr Ser Arg Val Lys Pro Asp  
                           195                          200                          205  
 Pro Pro His Ile Lys Asn Leu Ser Phe His Asn Asp Asp Leu Tyr Val  
           210                          215                          220  
 Gln Trp Glu Asn Pro Gln Asn Phe Ile Ser Arg Cys Leu Phe Tyr Glu  
 225                          230                          235                          240  
 Val Glu Val Asn Asn Ser Gln Thr Glu Thr His Asn Val Phe Tyr Val  
                           245                          250                          255  
 Gln Glu Ala Lys Cys Glu Asn Pro Glu Phe Glu Arg Asn Val Glu Asn  
                           260                          265                          270  
 Thr Ser Cys Phe Met Val Pro Gly Val Leu Pro Asp Thr Leu Asn Thr  
           275                          280                          285  
 Val Arg Ile Arg Val Lys Thr Asn Lys Leu Cys Tyr Glu Asp Asp Lys  
           290                          295                          300  
 Leu Trp Ser Asn Trp Ser Gln Glu Met Ser Ile Gly Lys Lys Arg Asn  
 305                          310                          315                          320  
 Ser Thr

<210> 83  
 <211> 951  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)...(951)

<400> 83

gac acc gag ata aaa gtt aac cct cct cag gat ttt gag ata gtg gat  
 Asp Thr Glu Ile Lys Val Asn Pro Pro Gln Asp Phe Glu Ile Val Asp  
 1                          5                          10                          15

ccc gga tac tta ggt tat ctc tat ttg caa tgg caa ccc cca ctg tct Pro Gly Tyr Leu Gly Tyr Leu Tyr Leu Gln Trp Gln Pro Pro Leu Ser 20 25 30	96
ctg gat cat ttt aag gaa tgc aca gtg gaa tat gaa cta aaa tac cga Leu Asp His Phe Lys Glu Cys Thr Val Glu Tyr Glu Leu Lys Tyr Arg 35 40 45	144
aac att ggt agt gaa aca tgg aag acc atc att act aag aat cta cat Asn Ile Gly Ser Glu Thr Trp Lys Thr Ile Ile Thr Lys Asn Leu His 50 55 60	192
tac aaa gat ggg ttt gat ctt aac aag ggc att gaa gcg aag ata cac Tyr Lys Asp Gly Phe Asp Leu Asn Lys Gly Ile Glu Ala Lys Ile His 65 70 75 80	240
acg ctt tta cca tgg caa tgc aca aat gga tca gaa gtt caa agt tcc Thr Leu Leu Pro Trp Gln Cys Thr Asn Gly Ser Glu Val Gln Ser Ser 85 90 95	288
tgg gca gaa act act tat tgg ata tca cca caa gga att cca gaa act Trp Ala Glu Thr Thr Tyr Trp Ile Ser Pro Gln Gly Ile Pro Glu Thr 100 105 110	336
aaa gtt cag gat atg gat tgc gta tat tac aat tgg caa tat tta ctc Lys Val Gln Asp Met Asp Cys Val Tyr Tyr Asn Trp Gln Tyr Leu Leu 115 120 125	384
tgt tct tgg aaa cct ggc ata ggt gta ctt ctt gat acc aat tac aac Cys Ser Trp Lys Pro Gly Ile Gly Val Leu Leu Asp Thr Asn Tyr Asn 130 135 140	432
ttg ttt tac tgg tat gag ggc ttg gat cat gca tta cag tgt gtt gat Leu Phe Tyr Trp Tyr Glu Gly Leu Asp His Ala Leu Gln Cys Val Asp 145 150 155 160	480
tac atc aag gct gat gga caa aat ata gga tgc aga ttt ccc tat ttg Tyr Ile Lys Ala Asp Gly Gln Asn Ile Gly Cys Arg Phe Pro Tyr Leu 165 170 175	528
gag gca tca gac tat aaa gat ttc tat att tgt gtt aat gga tca tca Glu Ala Ser Asp Tyr Lys Asp Phe Tyr Ile Cys Val Asn Gly Ser Ser 180 185 190	576



gag aac aag cct atc aga tcc agt tat ttc act ttt cag ctt caa aat	624
Glu Asn Lys Pro Ile Arg Ser Ser Tyr Phe Thr Phe Gln Leu Gln Asn	
195 200 205	
ata gtt aaa cct ttg ccg cca gtc tat ctt act ttt act cgg gag agt	672
Ile Val Lys Pro Leu Pro Pro Val Tyr Leu Thr Phe Thr Arg Glu Ser	
210 215 220	
tca tgt gaa att aag ctg aaa tgg agc ata cct ttg gga cct att cca	720
Ser Cys Glu Ile Lys Leu Lys Trp Ser Ile Pro Leu Gly Pro Ile Pro	
225 230 235 240	
gca agg tgt ttt gat tat gaa att gag atc aga gaa gat gat act acc	768
Ala Arg Cys Phe Asp Tyr Glu Ile Glu Ile Arg Glu Asp Asp Thr Thr	
245 250 255	
ttg gtg act gct aca gtt gaa aat gaa aca tac acc ttg aaa aca aca	816
Leu Val Thr Ala Thr Val Glu Asn Glu Thr Tyr Thr Leu Lys Thr Thr	
260 265 270	
aat gaa acc cga caa tta tgc ttt gta gta aga agc aaa gtg aat att	864
Asn Glu Thr Arg Gln Leu Cys Phe Val Val Arg Ser Lys Val Asn Ile	
275 280 285	
tat tgc tca gat gac gga att tgg agt gag tgg agt gat aaa caa tgc	912
Tyr Cys Ser Asp Asp Gly Ile Trp Ser Glu Trp Ser Asp Lys Gln Cys	
290 295 300	
tgg gaa ggt gaa gac cta tcg aag aaa act ttg cta cgt	951
Trp Glu Gly Glu Asp Leu Ser Lys Lys Thr Leu Leu Arg	
305 310 315	

&lt;210&gt; 84

&lt;211&gt; 317

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 84

Asp Thr Glu Ile Lys Val Asn Pro Pro Gln Asp Phe Glu Ile Val Asp
1 5 10 15

Pro	Gly	Tyr	Leu	Gly	Tyr	Leu	Tyr	Leu	Gln	Trp	Gln	Pro	Pro	Leu	Ser
			20					25					30		
Leu	Asp	His	Phe	Lys	Glu	Cys	Thr	Val	Glu	Tyr	Glu	Leu	Lys	Tyr	Arg
		35					40					45			
Asn	Ile	Gly	Ser	Glu	Thr	Trp	Lys	Thr	Ile	Ile	Thr	Lys	Asn	Leu	His
	50					55					60				
Tyr	Lys	Asp	Gly	Phe	Asp	Leu	Asn	Lys	Gly	Ile	Glu	Ala	Lys	Ile	His
65					70					75					80
Thr	Leu	Leu	Pro	Trp	Gln	Cys	Thr	Asn	Gly	Ser	Glu	Val	Gln	Ser	Ser
				85					90					95	
Trp	Ala	Glu	Thr	Thr	Tyr	Trp	Ile	Ser	Pro	Gln	Gly	Ile	Pro	Glu	Thr
			100					105					110		
Lys	Val	Gln	Asp	Met	Asp	Cys	Val	Tyr	Tyr	Asn	Trp	Gln	Tyr	Leu	Leu
		115					120					125			
Cys	Ser	Trp	Lys	Pro	Gly	Ile	Gly	Val	Leu	Leu	Asp	Thr	Asn	Tyr	Asn
	130					135					140				
Leu	Phe	Tyr	Trp	Tyr	Glu	Gly	Leu	Asp	His	Ala	Leu	Gln	Cys	Val	Asp
145					150					155					160
Tyr	Ile	Lys	Ala	Asp	Gly	Gln	Asn	Ile	Gly	Cys	Arg	Phe	Pro	Tyr	Leu
				165					170					175	
Glu	Ala	Ser	Asp	Tyr	Lys	Asp	Phe	Tyr	Ile	Cys	Val	Asn	Gly	Ser	Ser
			180					185					190		
Glu	Asn	Lys	Pro	Ile	Arg	Ser	Ser	Tyr	Phe	Thr	Phe	Gln	Leu	Gln	Asn
	195						200					205			
Ile	Val	Lys	Pro	Leu	Pro	Pro	Val	Tyr	Leu	Thr	Phe	Thr	Arg	Glu	Ser
	210					215						220			
Ser	Cys	Glu	Ile	Lys	Leu	Lys	Trp	Ser	Ile	Pro	Leu	Gly	Pro	Ile	Pro
225					230					235					240
Ala	Arg	Cys	Phe	Asp	Tyr	Glu	Ile	Glu	Ile	Arg	Glu	Asp	Asp	Thr	Thr
				245					250					255	
Leu	Val	Thr	Ala	Thr	Val	Glu	Asn	Glu	Thr	Tyr	Thr	Leu	Lys	Thr	Thr
			260					265					270		
Asn	Glu	Thr	Arg	Gln	Leu	Cys	Phe	Val	Val	Arg	Ser	Lys	Val	Asn	Ile
		275					280					285			
Tyr	Cys	Ser	Asp	Asp	Gly	Ile	Trp	Ser	Glu	Trp	Ser	Asp	Lys	Gln	Cys
	290					295					300				
Trp	Glu	Gly	Glu	Asp	Leu	Ser	Lys	Lys	Thr	Leu	Leu	Arg			
305					310						315				

&lt;210&gt; 85

&lt;211&gt; 519

&lt;212&gt; DNA

&lt;213&gt; Homo sapeins

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(519)

&lt;400&gt; 85

atc	acg	tgc	cct	ccc	ccc	atg	tcc	gtg	gaa	cac	gca	gac	atc	tgg	gtc	48
Ile	Thr	Cys	Pro	Pro	Pro	Met	Ser	Val	Glu	His	Ala	Asp	Ile	Trp	Val	
1				5				10						15		

aag	agc	tac	agc	ttg	tac	tcc	agg	gag	cgg	tac	att	tgt	aac	tct	ggt	96
Lys	Ser	Tyr	Ser	Leu	Tyr	Ser	Arg	Glu	Arg	Tyr	Ile	Cys	Asn	Ser	Gly	
			20					25					30			

ttc	aag	cgt	aaa	gcc	ggc	acg	tcc	agc	ctg	acg	gag	tgc	gtg	ttg	aac	144
Phe	Lys	Arg	Lys	Ala	Gly	Thr	Ser	Ser	Leu	Thr	Glu	Cys	Val	Leu	Asn	
		35					40					45				

aag	gcc	acg	aat	gtc	gcc	cac	tgg	aca	acc	ccc	agt	ctc	aaa	tgc	att	192
Lys	Ala	Thr	Asn	Val	Ala	His	Trp	Thr	Thr	Pro	Ser	Leu	Lys	Cys	Ile	
	50					55					60					

aga	gac	cct	gcc	ctg	gtt	cac	caa	agg	cca	gcg	cca	ccc	tcc	aca	gta	240
Arg	Asp	Pro	Ala	Leu	Val	His	Gln	Arg	Pro	Ala	Pro	Pro	Ser	Thr	Val	
65				70					75						80	

acg	acg	gca	ggg	gtg	acc	cca	cag	cca	gag	agc	ctc	tcc	cct	tct	gga	288
Thr	Thr	Ala	Gly	Val	Thr	Pro	Gln	Pro	Glu	Ser	Leu	Ser	Pro	Ser	Gly	
			85						90					95		

aaa	gag	ccc	gca	gct	tca	tct	ccc	agc	tca	aac	aac	aca	gcg	gcc	aca	336
Lys	Glu	Pro	Ala	Ala	Ser	Ser	Pro	Ser	Ser	Asn	Asn	Thr	Ala	Ala	Thr	
			100					105					110			

aca	gca	gct	att	gtc	ccg	ggc	tcc	cag	ctg	atg	cct	tca	aaa	tca	cct	384
Thr	Ala	Ala	Ile	Val	Pro	Gly	Ser	Gln	Leu	Met	Pro	Ser	Lys	Ser	Pro	
		115					120					125				

tcc	aca	gga	acc	aca	gag	ata	agc	agt	cat	gag	tcc	tcc	cac	ggc	acc	432
Ser	Thr	Gly	Thr	Thr	Glu	Ile	Ser	Ser	His	Glu	Ser	Ser	His	Gly	Thr	
	130					135					140					

ccc tct cag aca aca gcc aag aac tgg gaa ctc aca gca tcc gcc tcc 480  
 Pro Ser Gln Thr Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala Ser  
 145 150 155 160

cac cag ccg cca ggt gtg tat cca cag ggc cac agc gac 519  
 His Gln Pro Pro Gly Val Tyr Pro Gln Gly His Ser Asp  
 165 170

<210> 86

<211> 173

<212> PRT

<213> Homo sapeins

<400> 86

Ile Thr Cys Pro Pro Pro Met Ser Val Glu His Ala Asp Ile Trp Val  
 1 5 10 15  
 Lys Ser Tyr Ser Leu Tyr Ser Arg Glu Arg Tyr Ile Cys Asn Ser Gly  
 20 25 30  
 Phe Lys Arg Lys Ala Gly Thr Ser Ser Leu Thr Glu Cys Val Leu Asn  
 35 40 45  
 Lys Ala Thr Asn Val Ala His Trp Thr Thr Pro Ser Leu Lys Cys Ile  
 50 55 60  
 Arg Asp Pro Ala Leu Val His Gln Arg Pro Ala Pro Pro Ser Thr Val  
 65 70 75 80  
 Thr Thr Ala Gly Val Thr Pro Gln Pro Glu Ser Leu Ser Pro Ser Gly  
 85 90 95  
 Lys Glu Pro Ala Ala Ser Ser Pro Ser Ser Asn Asn Thr Ala Ala Thr  
 100 105 110  
 Thr Ala Ala Ile Val Pro Gly Ser Gln Leu Met Pro Ser Lys Ser Pro  
 115 120 125  
 Ser Thr Gly Thr Thr Glu Ile Ser Ser His Glu Ser Ser His Gly Thr  
 130 135 140  
 Pro Ser Gln Thr Thr Ala Lys Asn Trp Glu Leu Thr Ala Ser Ala Ser  
 145 150 155 160  
 His Gln Pro Pro Gly Val Tyr Pro Gln Gly His Ser Asp  
 165 170